

## REMARKS

The specification has been amended to recite the priority data, to amend various paragraphs to correct typographical errors, to include sequence identifiers for amino acid sequences disclosed in the specification, to cancel claims 1-37 of the PCT application, and to add new claims 38-60. Support for the new claims is found in the specification and claims as originally filed. In addition, the specification has been amended to replace the Sequence Listing with a substitute Sequence Listing that includes two additional sequences disclosed in the specification.

No new matter is added by this amendment. The filing fee has been calculated after amendment of the claims by the preliminary amendment.

Should any additional fees under 37 C.F.R. §§ 1.16 to 1.21 be required, the Commissioner is hereby authorized to deduct said fees from Fulbright & Jaworski Deposit Account No. 50-1212/SONN:078US.

Respectfully submitted,

  
for Mark B. Wilson  
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10/551492  
JC09 Rec'd PCT/PTO 30 SEP 2005

## APPENDIX A

SEQUENCE LISTING

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 <213> *Staphylococcus epidermidis*

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 <213> *Staphylococcus epidermidis*

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2391

<211> 987  
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<213> *Staphylococcus epidermidis*

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 <213> *Staphylococcus epidermidis*

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 <213> *Staphylococcus epidermidis*

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 <213> *Staphylococcus epidermidis*

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 <212> DNA  
 <213> *Staphylococcus epidermidis*

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ccacatttag atacacgtta tatkgttgg gaaagaacat tattatttgg accatttgca	960
aatattggcc ctaaattctt aagaaacggt tctaacttag acttattcaa atcagttaaa	1020
ccttataaca tcacaacatt actagcatct gcagttaaaa acttaccttt aatcaaatac	1080
tctatcgacc aagtattaaat gactaaagaa ggttgtatga accatctacg cacgttctac	1140
cctgaagctc gtgacgaaga ttggcaatta tacactgcag gtaaacgtgt tcaagttatc	1200
aaagatacta aagaacacgg taaaggattc attcaattt gtagacaatg tttactct	1260
aaagaccact ctgttatcgc actattgggt gaatcacctg gagcatcaac ttcagtatca	1320
gtagccctag aagttttaga gaaaaacttt gctgagttatg aaaaagattt gactccaaa	1380
ttacaaaaaa tgatccatc atatggtaaa tctcttatcg atgatgtttaa gttatgaga	1440
gcaactcgta aacaacatc taaagattt gaattaaatt attacgaatc taaa	1494

<210> 28  
 <211> 1548  
 <212> DNA  
 <213> *Staphylococcus epidermidis*

<400> 28	
atgaaaaat taaaaacttt aagttctata ctagttacat ctgttcttc tgtgactgt	60
attccctcaa catttgcattc aacagaatct actgctacaa atcagacaca acaaacagta	120
ctttttgata attctcatgc tcaaactgcg ggcgctgccg attgggtat tgatggcgct	180
ttctcagatt atgcagattc aatgagaaaag caaggttacc aagttaaaga actagaagga	240
gaatcaaaca tttctgatca atctttacag caggcgcatg tattagttat tcccgaagct	300
aacaatccat taaagaaaa tgagcagaaa gcaatcatta atttgtttaa aaatgggtgt	360

agcgtcatt	tcatctcaga	ccattataat	gccgatcgta	attnaaatcg	tattgattct	420
tcagaatcaa	tgaatggta	tcgacgtggc	gcatacgaaa	atatgactaa	agatatgaat	480
aatgaagaaa	agaattctaa	cgttatgcat	aacgttaaga	gttctgattg	gctctcacaa	540
aacttcggtg	ttcgctttag	atataatgca	cttggagata	tcaatactca	aaatatcggt	600
tcaagcaaag	atagtttgg	tattactaaa	ggtgtacaat	cagtttcgat	gcacgcaggt	660
tcaacattag	caataactga	tcctaataaa	gctaaaggca	ttatttatat	gccggaacat	720
ttaacgcata	gtcaaaaatg	gcctcacgca	gttgatcaag	gtatttacaa	tggggggtggc	780
atcaacgaag	gaccttatgt	agccatttca	aaaatcgga	aaggtaaagc	tgcatttatt	840
ggcgatagct	ccctcgtaga	agatcggtca	cctaaatatac	ttcgtgaaga	taatgggaaa	900
cctaaaaaaaaa	cgtacgatgg	ttttaaagaa	caagataatg	gaaagttatt	aaataattta	960
acaacatggc	taggaaaaaaaa	agaatctcaa	tcttctatga	aagacatggg	gattaaactt	1020
gataataaaaa	caccgctact	taactttgag	caacctgaga	attcaattga	acctcaaaaa	1080
gaaccgtgga	ctaaccatat	agaaggttac	aaatggtatg	atcggtcaac	atttaaaaca	1140
ggtagttatg	gaagtaatca	acggggtgct	gacgatggag	tagatgacaa	aagctcttct	1200
catcaaaatc	aaaatgccaa	agttgaatta	actttacctc	aaaatatcca	accgcacatcat	1260
ccatttcaat	ttacaatcaa	actcacggg	tatgagccta	atagcacaat	tagcgatgt	1320
agagttggac	tttataaaga	tggaggttaag	caaatcggt	gctttcttc	taaccgtaac	1380
caattcaata	ctctcggcta	tagtcctggc	caatcaatta	aagcaaatgg	tgcggtgaa	1440
gcttcattca	cactcacagc	taaagtgaca	gatgaaatta	aagatgctaa	tattcgtgtt	1500
aaacaaggga	aaaaaattct	attaactcaa	aaaatgaatg	aaaatttt		1548

<210> 29  
 <211> 252  
 <212> DNA  
 <213> *Staphylococcus epidermidis*

<400> 29	ggtacaccat	tagaattagt	ttttgtcaat	actttaggac	ctaaaccttg	tttcgctaaa	60
	ccaaataaaaa	ttctactatt	agaatatatt	ccgctatttg	ttgcagatgc	tgctgctgtt	120
	aaaacaacaa	aattaactat	gccagcagca	aaggaaacac	caattagtgt	gaataattta	180
	acaaaacggac	tactatcagg	atcaacttta	aaccatggaa	tgacagacat	gattacaagt	240
	aaaccaccta	ta					252

<210> 30  
 <211> 162

<212> DNA  
 <213> *Staphylococcus epidermidis*

<400> 30  
 tcatcgtaa gtaccataat tcctttct ttaggagcat taggcaaatt taattcttc 60  
 attgagcaaa tcataccact agaatctacc ccacgtaatt gggcatctt aattaccatt 120  
 ccgcttggca taacggcccc aactttgca acaacgacct tc 162

<210> 31  
 <211> 348  
 <212> DNA  
 <213> *Staphylococcus aureus*

<400> 31  
 atgaaaattta aaaaatataat attaacagga acattagcat tactttatc atcaactggg 60  
 atagcaacta tagaaggaa taaagcagat gcaagtagtc tggacaaata tttaactgaa 120  
 agtcagttc atgataaacg catagcagaa gaattaagaa cttaactttaa caaatcgaat 180  
 gtatatgcat tagctgcagg aagcttaat ccatattata aacgtacgat tatgatgaat 240  
 gaatatagag ctaaagcggc acttaagaaa aatgatttcg tatcaatggc tgatgctaaa 300  
 gttgcattag aaaaaatata caaagaaatt gatgaaatta taaataga 348

<210> 32  
 <211> 676  
 <212> PRT  
 <213> *Staphylococcus epidermidis*

<400> 32

Met	Lys	Arg	Thr	Asp	Lys	Ile	Gly	Val	Tyr	Leu	Lys	Leu	Ser	Cys	Ser
1					5				10					15	

Ala Leu Leu Leu Ser Gly Ser Leu Val Gly Tyr Gly Phe Thr Lys Asp  
 20 25 30

Ala Phe Ala Asp Ser Glu Ser Thr Ser Ser Asn Val Glu Asn Thr Ser  
 35 40 45

Asn Ser Asn Ser Ile Ala Asp Lys Ile Gln Gln Ala Lys Asp Asp Ile  
 50 55 60

Lys Asp Leu Lys Glu Leu Ser Asp Ala Asp Ile Lys Ser Phe Glu Glu  
 65 70 75 80

Arg Leu Asp Lys Val Asp Asn Gln Ser Ser Ile Asp Arg Ile Ile Asn  
 85 90 95

Asp Ala Lys Asp Lys Asn Asn His Leu Lys Ser Thr Asp Ser Ser Ala  
100 105 110

Thr Ser Ser Lys Thr Glu Asp Asp Asp Thr Ser Glu Lys Asp Asn Asp  
115 120 125

Asp Met Thr Lys Asp Leu Asp Lys Ile Leu Ser Asp Leu Asp Ser Ile  
130 135 140

Ala Lys Asn Val Asp Asn Arg Gln Gln Gly Glu Glu Arg Ala Ser Lys  
145 150 155 160

Pro Ser Asp Ser Thr Thr Asp Glu Lys Asp Asp Ser Asn Asn Lys Val  
165 170 175

His Asp Thr Asn Ala Ser Thr Arg Asn Ala Thr Thr Asp Asp Ser Glu  
180 185 190

Glu Ser Val Ile Asp Lys Leu Asp Lys Ile Gln Gln Asp Phe Lys Ser  
195 200 205

Asp Ser Asn Asn Asn Pro Ser Glu Gln Ser Asp Gln Gln Ala Ser Pro  
210 215 220

Ser Asn Lys Thr Glu Asn Asn Lys Glu Glu Ser Ser Thr Thr Thr Asn  
225 230 235 240

Gln Ser Asp Ser Asp Ser Lys Asp Asp Lys Ser Asn Asp Gly His Arg  
245 250 255

Ser Thr Leu Glu Arg Ile Ala Ser Asp Thr Asp Gln Ile Arg Asp Ser  
260 265 270

Lys Asp Gln His Val Thr Asp Glu Lys Gln Asp Ile Gln Ala Ile Thr  
275 280 285

Arg Ser Leu Gln Gly Ser Asp Lys Ile Glu Lys Ala Leu Ala Lys Val  
290 295 300

Gln Ser Asp Asn Gln Ser Leu Asp Ser Asn Tyr Ile Asn Asn Lys Leu  
305 310 315 320

Met Asn Leu Arg Ser Leu Asp Thr Lys Val Glu Asp Asn Asn Thr Leu  
325 330 335

Ser Asp Asp Lys Lys Gln Ala Leu Lys Gln Glu Ile Asp Lys Thr Lys

340

345

350

Gln Ser Ile Asp Arg Gln Arg Asn Ile Ile Ile Asp Gln Leu Asn Gly  
355 360 365

Ala Ser Asn Lys Lys Gln Ala Thr Glu Asp Ile Leu Asn Ser Val Phe  
370 375 380

Ser Lys Asn Glu Val Glu Asp Ile Met Lys Arg Ile Lys Thr Asn Gly  
385 390 395 400

Arg Ser Asn Glu Asp Ile Ala Asn Gln Ile Ala Lys Gln Ile Asp Gly  
405 410 415

Leu Ala Leu Thr Ser Ser Asp Asp Ile Leu Lys Ser Met Leu Asp Gln  
420 425 430

Ser Lys Asp Lys Glu Ser Leu Ile Lys Gln Leu Leu Thr Thr Arg Leu  
435 440 445

Gly Asn Asp Glu Ala Asp Arg Ile Ala Lys Lys Leu Leu Ser Gln Asn  
450 455 460

Leu Ser Asn Ser Gln Ile Val Glu Gln Leu Lys Arg His Phe Asn Ser  
465 470 475 480

Gln Gly Thr Ala Thr Ala Asp Asp Ile Leu Asn Gly Val Ile Asn Asp  
485 490 495

Ala Lys Asp Lys Arg Gln Ala Ile Glu Thr Ile Leu Gln Thr Arg Ile  
500 505 510

Asn Lys Asp Lys Ala Lys Ile Ile Ala Asp Val Ile Ala Arg Val Gln  
515 520 525

Lys Asp Lys Ser Asp Ile Met Asp Leu Ile His Ser Ala Ile Glu Gly  
530 535 540

Lys Ala Asn Asp Leu Leu Asp Ile Glu Lys Arg Ala Lys Gln Ala Lys  
545 550 555 560

Lys Asp Leu Glu Tyr Ile Leu Asp Pro Ile Lys Asn Arg Pro Ser Leu  
565 570 575

Leu Asp Arg Ile Asn Lys Gly Val Gly Asp Ser Asn Ser Ile Phe Asp  
580 585 590

Arg Pro Ser Leu Leu Asp Lys Leu His Ser Arg Gly Ser Ile Leu Asp  
595 600 605

Lys Leu Asp His Ser Ala Pro Glu Asn Gly Leu Ser Leu Asp Asn Lys  
610 615 620

Gly Gly Leu Leu Ser Asp Leu Phe Asp Asp Asp Gly Asn Ile Ser Leu  
625 630 635 640

Pro Ala Thr Gly Glu Val Ile Lys Gln His Trp Ile Pro Val Ala Val  
645 650 655

Val Leu Met Ser Leu Gly Gly Ala Leu Ile Phe Met Ala Arg Arg Lys  
660 665 670

Lys His Gln Asn  
675

<210> 33  
<211> 655  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 33

Met Lys Lys Asn Lys Phe Leu Val Tyr Leu Leu Ser Thr Ala Leu Ile  
1 5 10 15

Thr Pro Thr Phe Ala Thr Gln Thr Ala Phe Ala Glu Asp Ser Ser Asn  
20 25 30

Lys Asn Thr Asn Ser Asp Lys Met Glu Gln His Gln Ser Gln Lys Glu  
35 40 45

Thr Ser Lys Gln Ser Glu Lys Asp Glu Phe Asn Asn Asp Asp Ser Lys  
50 55 60

His Asp Ser Asp Asp Lys Lys Ser Thr Ser Asp Ser Lys Asp Lys Asp  
65 70 75 80

Ser Asn Lys Pro Leu Ser Ala Asp Ser Thr His Arg Asn Tyr Lys Met  
85 90 95

Lys Asp Asp Asn Leu Val Asp Gln Leu Tyr Asp Asn Phe Lys Ser Gln  
100 105 110

Ser Val Asp Phe Ser Lys Tyr Trp Glu Pro Asn Lys Tyr Glu Asp Ser  
115 120 125

Phe Ser Leu Thr Ser Leu Ile Gln Asn Leu Phe Asp Phe Asp Ser Asp  
130 135 140

Ile Thr Asp Tyr Glu Gln Pro Gln Lys Thr Ser His Ser Ser Asn Asp  
145 150 155 160

Glu Lys Asp Gln Val Asp Gln Ala Asp Gln Ala Lys Gln Pro Ser Gln  
165 170 175

His Gln Glu Pro Ser Gln Ser Ser Ala Lys Gln Asp Gln Glu Pro Ser  
180 185 190

Asn Asp Glu Lys Glu Lys Thr Thr Asn His Gln Ala Asp Ser Asp Val  
195 200 205

Ser Asp Leu Leu Gly Glu Met Asp Lys Glu Asp Gln Glu Gly Glu Asn  
210 215 220

Val Asp Thr Asn Lys Asn Gln Ser Ser Ser Glu Gln Gln Gln Thr Gln  
225 230 235 240

Ala Asn Asp Asp Ser Ser Glu Arg Asn Lys Lys Tyr Ser Ser Ile Thr  
245 250 255

Asp Ser Ala Leu Asp Ser Ile Leu Asp Glu Tyr Ser Gln Asp Ala Lys  
260 265 270

Lys Thr Glu Lys Asp Tyr Asn Lys Ser Lys Asn Thr Ser His Thr Lys  
275 280 285

Thr Ser Gln Ser Asp Asn Ala Asp Lys Asn Pro Gln Leu Pro Thr Asp  
290 295 300

Asp Glu Leu Lys His Gln Ser Lys Pro Ala Gln Ser Phe Glu Asp Asp  
305 310 315 320

Ile Lys Arg Ser Asn Thr Arg Ser Thr Ser Leu Phe Gln Gln Leu Pro  
325 330 335

Glu Leu Asp Asn Gly Asp Leu Ser Ser Asp Ser Phe Asn Val Val Asp  
340 345 350

Ser Gln Asp Thr Arg Asp Phe Ile Gln Ser Ile Ala Lys Asp Ala His

355

360

365

Gln Ile Gly Lys Asp Gln Asp Ile Tyr Ala Ser Val Met Ile Ala Gln  
 370 375 380

Ala Ile Leu Glu Ser Asp Ser Gly Lys Ser Ser Leu Ala Gln Ser Pro  
 385 390 395 400

Asn His Asn Leu Phe Gly Ile Lys Gly Asp Tyr Lys Gly Gln Ser Val  
 405 410 415

Thr Phe Asn Thr Leu Glu Ala Asp Ser Ser Asn His Met Phe Ser Ile  
 420 425 430

Gln Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Gln Ser Leu Glu Asp  
 435 440 445

Tyr Ala Asp Leu Ile Lys His Gly Ile Asp Gly Asn Pro Ser Ile Tyr  
 450 455 460

Lys Pro Thr Trp Lys Ser Glu Ala Leu Ser Tyr Lys Asp Ala Thr Ser  
 465 470 475 480

His Leu Ser Arg Ser Tyr Ala Thr Asp Pro Asn Tyr Ser Lys Lys Leu  
 485 490 495

Asn Ser Ile Ile Lys His Tyr His Leu Thr Ser Phe Asp Lys Glu Lys  
 500 505 510

Met Pro Asn Met Lys Lys Tyr Asn Lys Ser Ile Gly Thr Asp Val Ser  
 515 520 525

Gly Asn Asp Phe Lys Pro Phe Thr Glu Thr Ser Gly Thr Ser Pro Tyr  
 530 535 540

Pro His Gly Gln Cys Thr Trp Tyr Val Tyr His Arg Met Asn Gln Phe  
 545 550 555 560

Asp Ala Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn  
 565 570 575

Arg Ala Glu Ser Glu Gly Tyr Thr Val Thr His Thr Pro Lys Asn His  
 580 585 590

Thr Ala Val Val Phe Glu Ala Gly Gln Leu Gly Ala Asp Thr Gln Tyr  
 595 600 605

Gly His Val Ala Phe Val Glu Lys Val Asn Asp Asp Gly Ser Ile Val  
610 615 620

Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Val Ile Ser Phe Arg Thr  
625 630 635 640

Ile Asp Ala Gly Asp Ala Gln Asp Leu Asp Tyr Ile Lys Gly Lys  
645 650 655

<210> 34  
<211> 164  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 34

Met Ile Arg Phe Ala Arg Leu Glu Asp Leu Gln Asp Ile Leu Thr Ile  
1 5 10 15

Tyr Asn Asp Ala Ile Leu Asn Thr Thr Ala Val Tyr Thr Tyr Lys Pro  
20 25 30

Gln Gln Leu Asp Glu Arg Leu Gln Trp Tyr Gln Ser Lys Ala Lys Ile  
35 40 45

Asn Glu Pro Ile Trp Val Tyr Glu Lys Glu Gly Lys Val Val Gly Phe  
50 55 60

Ala Thr Tyr Gly Ser Phe Arg Gln Trp Pro Ala Tyr Leu Tyr Thr Ile  
65 70 75 80

Glu His Ser Ile Tyr Val His Gln Gln Tyr Arg Gly Leu Gly Ile Ala  
85 90 95

Ser Gln Leu Leu Glu Asn Leu Ile Arg Tyr Ala Lys Glu Gln Gly Tyr  
100 105 110

Arg Thr Ile Val Ala Gly Ile Asp Ala Ser Asn Met Asp Ser Ile Ala  
115 120 125

Leu His Lys Lys Phe Asp Phe Ser His Ala Gly Thr Ile Lys Asn Val  
130 135 140

Gly Tyr Lys Phe Asp Arg Trp Leu Asp Leu Ser Phe Tyr Gln Tyr Asp  
145 150 155 160

Leu Ser Asp Ser

<210> 35  
<211> 952  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 35

Leu Ser Asn Leu Ile Gln Asp Ile Lys Gln Ser Leu Tyr Lys Gly Phe  
1 5 10 15

Ile Asp Lys Asp Ser Ser His Lys Gly Asn Phe Val Pro Arg Leu Leu  
20 25 30

Val Asn Asn Lys Glu Glu Asn Val Leu Ser Thr Ile Ile Asp Gln Leu  
35 40 45

His Asn Cys Gln Ser Phe Cys Ile Ser Val Ala Phe Ile Thr Glu Ser  
50 55 60

Gly Leu Ala Ser Leu Lys Ser His Phe Tyr Asp Leu Ser Lys Lys Gly  
65 70 75 80

Val Lys Gly Arg Ile Ile Thr Ser Asn Tyr Leu Gly Phe Asn Ser Pro  
85 90 95

Lys Met Phe Glu Glu Leu Leu Lys Leu Glu Asn Val Glu Val Lys Leu  
100 105 110

Thr Asn Ile Glu Gly Phe His Ala Lys Gly Tyr Ile Phe Glu His His  
115 120 125

Asn His Thr Ser Phe Ile Ile Gly Ser Ser Asn Leu Thr Ser Asn Ala  
130 135 140

Leu Lys Leu Asn Tyr Glu His Asn Leu Phe Leu Ser Thr His Lys Asn  
145 150 155 160

Gly Asp Leu Val Asn Asn Ile Lys Tyr Lys Phe Asp Glu Leu Trp Asp  
165 170 175

Ser Ser Phe Ser Leu Thr Asn Glu Trp Ile Asn Glu Tyr Lys Gln Ser  
180 185 190

Phe Glu Tyr Gln Thr Leu Gln Lys Val Phe Asp Asn Thr Val Val Gln  
195 200 205

Asn Ser Asp Ile Lys Lys Phe Asn Glu Ser Lys Leu Ile Lys Pro Asn  
210 215 220

Leu Met Gln Glu His Ala Leu Lys Ser Leu Glu Ser Leu Arg Asn Val  
225 230 235 240

Gly Glu Glu Lys Gly Leu Ile Ser Ala Thr Gly Thr Gly Lys Thr  
245 250 255

Ile Leu Cys Ala Leu Asp Val Arg Ala Tyr Ser Pro Asp Lys Phe Leu  
260 265 270

Phe Ile Val His Asn Glu Gly Ile Leu Asn Arg Ala Ile Glu Glu Phe  
275 280 285

Lys Lys Val Phe Pro Tyr Glu Asp Glu Ser Asn Phe Gly Leu Leu Thr  
290 295 300

Gly Lys Arg Lys Asp His Asp Ala Lys Phe Leu Phe Ala Thr Ile Gln  
305 310 315 320

Thr Leu Ser Lys Lys Glu Asn Tyr Lys Leu Phe Asn Ser Asn His Phe  
325 330 335

Asp Tyr Ile Val Phe Asp Glu Ala His Arg Ile Ala Ala Ser Ser Tyr  
340 345 350

Gln Lys Ile Phe Asn Tyr Phe Lys Pro Asn Phe Leu Leu Gly Met Thr  
355 360 365

Ala Thr Pro Glu Arg Thr Asp Glu Leu Asn Ile Phe Glu Leu Phe Asn  
370 375 380

Tyr Asn Ile Ala Tyr Glu Ile Arg Leu Gln Glu Ala Leu Glu Ser Asn  
385 390 395 400

Ile Leu Cys Pro Phe His Tyr Phe Gly Val Thr Asp Tyr Ile Gln Asn  
405 410 415

Glu Met Ser Gln Glu Asp Ala Phe Asn Leu Lys Tyr Leu Ala Ser Asn  
420 425 430

Glu Arg Val Glu His Ile Ile Lys Lys Thr Asn Tyr Tyr Gly Tyr Ser  
435 440 445

Gly Asp Val Leu Lys Gly Leu Ile Phe Val Ser Ser Arg Gly Glu Ala  
450 455 460

Tyr Gln Leu Ala Asn Gln Leu Ser Lys Arg Gly Ile Ser Ser Val Gly  
465 470 475 480

Leu Thr Gly Lys Asp Ser Ile Ala Tyr Arg Ala Glu Thr Ile Gln Gln  
485 490 495

Leu Lys Glu Gly Ser Ile Asn Tyr Ile Ile Thr Val Asp Leu Phe Asn  
500 505 510

Glu Gly Ile Asp Ile Pro Glu Ile Asn Gln Val Val Met Leu Arg Pro  
515 520 525

Thr Lys Ser Ser Ile Ile Phe Ile Gln Gln Leu Gly Arg Gly Leu Arg  
530 535 540

Lys Ser Thr Asn Lys Glu Phe Val Thr Val Ile Asp Phe Ile Gly Asn  
545 550 555 560

Tyr Lys Thr Asn Tyr Met Ile Pro Ile Ala Leu Ser Gly Asn Lys Ser  
565 570 575

Gln Asn Lys Asp Asn Tyr Arg Lys Phe Leu Thr Asp Thr Thr Val Leu  
580 585 590

Asn Gly Val Ser Thr Ile Asn Phe Glu Glu Val Ala Lys Asn Lys Ile  
595 600 605

Tyr Asn Ser Leu Asp Ser Val Lys Leu Asn Gln Pro Lys Leu Ile Lys  
610 615 620

Glu Ala Phe Asn Asn Val Lys Asp Arg Ile Gly Lys Leu Pro Leu Leu  
625 630 635 640

Met Asp Phe Ile Asn Asn Asp Ser Ile Asp Pro Ser Val Ile Phe Ser  
645 650 655

Arg Phe Lys Asn Tyr Tyr Glu Phe Leu Ile Lys Asn Lys Ile Ile Glu  
660 665 670

Asn Glu Leu Ser Ile Asn Glu Phe Lys Asn Leu Thr Phe Leu Ser Arg  
675 680 685

Gln Leu Thr Pro Gly Leu Lys Lys Val Asp Ile Asp Val Leu Lys Glu  
690 695 700

Ile Ile Gln Asn Asp Val Thr Tyr Glu Asn Leu Thr Lys Lys Met Leu  
705 710 715 720

Asn Ile Asn Asn Asp Ile Ser Glu Tyr Asp Ile Asn Thr Ser Leu Ser  
725 730 735

Ile Leu Asp Phe Thr Phe Phe Lys Lys Thr Ile Gly Lys Thr Tyr Gly  
740 745 750

Leu Pro Leu Ile Gln Tyr Lys Asp Asn Leu Ile Cys Leu Ala Asn Glu  
755 760 765

Phe Lys Glu Ala Leu Asn Lys Pro Leu Phe Asn Thr Phe Ile His Asp  
770 775 780

Leu Ile Asp Leu Ala Asn Tyr Asn Asn Asp Arg Tyr Gln Asn Lys Lys  
785 790 795 800

Asn Ser Leu Ile Leu Tyr Asn Lys Tyr Ser Arg Glu Asp Phe Val Lys  
805 810 815

Leu Leu Asn Trp Asp Lys Asp Glu Ser Gly Thr Ile Asn Gly Tyr Arg  
820 825 830

Met Lys His Arg Thr Leu Pro Leu Phe Ile Thr Tyr Asp Lys His Glu  
835 840 845

Asn Ile Ser Asp Asn Thr Lys Tyr Asp Asp Glu Phe Leu Ser Gln Asp  
850 855 860

Glu Leu Lys Trp Tyr Thr Arg Ser Asn Arg Lys Leu Thr Ser Pro Glu  
865 870 875 880

Val Gln Asn Ile Leu Lys His Glu Glu Ser Asn Thr Asp Met Tyr Ile  
885 890 895

Phe Val Lys Lys Arg Asp Asp Glu Gly Lys Tyr Phe Tyr Tyr Leu Gly  
900 905 910

Lys Ala Lys Tyr Ile Lys Gly Thr Glu Lys Gln Asp Tyr Met Pro Asn  
915 920 925

Gly Asn Ser Val Val Thr Met His Leu Ser Met Asn Thr Ser Ile Arg

930

935

940

Asp Asp Ile Tyr Arg Tyr Ile Thr  
945 950

<210> 36  
<211> 325  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 36

Met Thr Lys Ser Gln Gln Lys Val Ser Ser Ile Glu Lys Leu Ser Asn  
1 5 10 15

Gln Glu Gly Ile Ile Ser Ala Leu Ala Phe Asp Gln Arg Gly Ala Leu  
20 25 30

Lys Arg Met Met Ala Glu His Gln Ser Glu Thr Pro Thr Val Glu Gln  
35 40 45

Ile Glu Gln Leu Lys Val Leu Val Ser Glu Glu Leu Thr Gln Tyr Ala  
50 55 60

Ser Ser Ile Leu Leu Asp Pro Glu Tyr Gly Leu Pro Ala Ser Asp Ala  
65 70 75 80

Arg Asn Asn Asp Cys Gly Leu Leu Ala Tyr Glu Lys Thr Gly Tyr  
85 90 95

Asp Val Asn Ala Lys Gly Arg Leu Pro Asp Cys Leu Val Glu Trp Ser  
100 105 110

Ala Lys Arg Leu Lys Glu Gln Gly Ala Asn Ala Val Lys Phe Leu Leu  
115 120 125

Tyr Tyr Asp Val Asp Asp Thr Glu Glu Ile Asn Ile Gln Lys Lys Ala  
130 135 140

Tyr Ile Glu Arg Ile Gly Ser Glu Cys Val Ala Glu Asp Ile Pro Phe  
145 150 155 160

Phe Leu Glu Val Leu Thr Tyr Asp Asp Asn Ile Pro Asp Asn Lys Ser  
165 170 175

Ala Glu Phe Ala Lys Val Lys Pro Arg Lys Val Asn Glu Ala Met Lys  
180 185 190

Leu Phe Ser Glu Asp Arg Phe Asn Val Asp Val Leu Lys Val Glu Val  
195 200 205

Pro Val Asn Met Asn Phe Val Glu Gly Phe Ser Glu Gly Glu Val Val  
210 215 220

Tyr Thr Lys Glu Glu Ala Ala Gln His Phe Arg Asp Gln Asp Ala Ala  
225 230 235 240

Thr His Leu Pro Tyr Ile Tyr Leu Ser Ala Gly Val Ser Ala Glu Leu  
245 250 255

Phe Gln Asp Thr Leu Lys Phe Ala His Asp Ser Gly Ala Gln Phe Asn  
260 265 270

Gly Val Leu Cys Gly Arg Ala Thr Trp Ser Gly Ala Val Lys Val Tyr  
275 280 285

Ile Glu Glu Gly Glu Gln Ala Ala Arg Glu Trp Leu Arg Thr Val Gly  
290 295 300

Phe Lys Asn Ile Asp Asp Leu Asn Thr Val Leu Lys Thr Thr Ala Thr  
305 310 315 320

Ser Trp Lys Asn Lys  
325

<210> 37  
<211> 382  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 37

Leu Met Lys Lys Val Met Thr Ile Phe Gly Thr Arg Pro Glu Ala Ile  
1 5 10 15

Lys Met Ala Pro Leu Ile Lys Thr Leu Glu Lys Asp Ser Asp Leu Glu  
20 25 30

Pro Val Val Val Val Thr Ala Gln His Arg Glu Met Leu Asp Ser Val  
35 40 45

Leu Asn Thr Phe Asn Ile Ser Ala Asp Tyr Asp Leu Asn Ile Met Lys  
50 55 60

Ala Gly Gln Thr Leu Ser Glu Val Thr Ser Glu Ala Met Lys Lys Leu

65

70

75

80

Glu Asp Ile Ile Gln Lys Glu Val Pro Asp Met Val Leu Val His Gly  
85 90 95

Asp Thr Val Thr Phe Ser Gly Ala Leu Ala Ala Phe Tyr Ser Gln  
100 105 110

Thr Pro Ile Gly His Val Glu Ala Gly Leu Arg Ser Tyr Asn Lys Tyr  
115 120 125

Ser Pro Tyr Pro Glu Glu Ile Asn Arg Gln Met Val Gly Val Met Ala  
130 135 140

Asp Leu His Phe Ala Pro Thr Tyr Asn Ala Ala Gln Asn Leu Val Lys  
145 150 155 160

Glu Gly Lys Leu Ala Lys His Ile Ala Ile Thr Gly Asn Thr Ala Ile  
165 170 175

Asp Ala Met Asn Tyr Thr Ile Asp His Gln Tyr Ser Ser Ile Ile  
180 185 190

Gln Lys His Lys Asn Lys Asn Phe Ile Leu Leu Thr Ala His Arg Arg  
195 200 205

Glu Asn Ile Gly Lys Pro Met Ile Asn Val Phe Lys Ala Ile Arg Lys  
210 215 220

Leu Ile Asp Glu Tyr Gln Asp Leu Ala Leu Val Tyr Pro Met His Met  
225 230 235 240

Asn Pro Lys Val Arg Asp Ile Ala Gln Lys Tyr Leu Gly Asn His Pro  
245 250 255

Arg Ile Glu Leu Ile Glu Pro Leu Asp Val Val Asp Phe His Asn Phe  
260 265 270

Ala Lys Gln Ala Tyr Leu Ile Met Thr Asp Ser Gly Gly Ile Gln Glu  
275 280 285

Glu Ala Pro Ser Leu His Lys Pro Val Leu Val Leu Arg Asp Ser Thr  
290 295 300

Glu Arg Pro Glu Gly Val Asp Ala Gly Thr Leu Arg Val Ile Gly Thr  
305 310 315 320

Asn Glu Glu Asp Val Tyr Asn Glu Thr Lys Lys Leu Ile Glu Asn Pro  
325 330 335

Asp Leu Tyr Gln Lys Met Ser Gln Ala Val Asn Pro Tyr Gly Asp Gly  
340 345 350

Gln Ala Ser Glu Arg Ile Val Gln His Ile Lys Tyr Tyr Phe Asn Leu  
355 360 365

Thr Asn Asp Arg Pro Asn His Phe Glu Phe Thr Lys Asp Leu  
370 375 380

<210> 38  
<211> 2757  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 38

Val Ala Ser Asp Phe Asn Ile Gly Ile Leu Ser Thr Leu Glu Ile Asp  
1 5 10 15

Ser Ser Ser Ser Arg Lys Lys Ile Asn Asp Thr Leu Lys Asn Ile Glu  
20 25 30

Ala Asn Ile Asn Ser Ile Lys Ala Asp Leu Glu Val Ser Asp Thr Lys  
35 40 45

Lys Ser Glu Asn Asn Ala Ile Lys Ser Ala Asn Asn Val Ile Arg Asn  
50 55 60

Ile Asn Ser Asn Gly Asn Leu Lys Lys Leu Asn Val Glu Leu Asp Val  
65 70 75 80

Asn Leu Thr Lys Ser Arg Gln Asn Ile Gln Arg Ala Leu Ser Thr Leu  
85 90 95

Ser Lys Asp Phe Lys Asn Lys Ile Asp Val Glu Val Asn Ala Lys  
100 105 110

Ala Asn Lys Asn Ser Ile Gly Gln Val Lys Asn Ser Ile Ser Lys Gly  
115 120 125

Ala Ser Gln Pro Leu Glu Ile Lys Glu Ser Pro Ser Ser Arg Ser Thr  
130 135 140

Ser Arg Asp Ile Lys Glu Gln Gln Ser Leu Met Thr Gly Leu Ala Asn  
145 150 155 160

Ser Tyr Lys Asn Leu Asp Asp Leu Thr Arg Ala Leu Asn Thr Ser Thr  
165 170 175

Phe Glu Gly Leu Arg Lys Thr Val Lys Glu Ile Lys Asn Ala Asp Asn  
180 185 190

Ser Leu Lys Ser Tyr Gln Val Thr Leu Glu Arg Val Asn Gln Glu Gly  
195 200 205

Lys Lys Leu Gly Ser Gln Arg Phe Asp Tyr Thr Pro Ser Ala Asn Gly  
210 215 220

Leu Lys Leu Asn Lys Thr Gln Leu Thr Asp Gln Thr Asp Lys Ala Arg  
225 230 235 240

Lys Glu Glu Asn Ala Ala Ile Asn Lys Leu Leu Glu Asn Glu Val Ser  
245 250 255

Lys Tyr Asp Arg Leu Leu Asn Lys Gly Lys Ile Asp Ile Lys Gln His  
260 265 270

Gln Thr Leu Leu Gln Thr Leu Arg Gln Ile Thr Asn Glu Lys Ser Lys  
275 280 285

Ala Asn Gln Phe Asn Arg Thr Asp Phe Asn Arg Val Ala Lys Ala Ala  
290 295 300

Ala Asp Glu Ala Lys Glu Tyr Gln Tyr Gln Asn Asp Met Leu Arg Lys  
305 310 315 320

Lys Leu Ala Leu Thr Ser Gln Ile Glu Arg Ile Glu Asn Arg Met Ala  
325 330 335

Ala Thr Ile Asp Lys Gln Gln Thr Asn Ala Leu Lys Asn Gln Leu Asn  
340 345 350

Ser Leu Gly Asn Asn Arg Thr Pro Phe Gly Lys Glu Ala Ala Phe His  
355 360 365

Met Asn Gln Ile Gln Asp Lys Val Arg Gln Ile Ser Ala Glu Ala Glu  
370 375 380

Arg Ala Thr Arg Thr Gln Leu Ser Phe Val Asp Gln Phe Arg Glu Ala

385

390

395

400

Met Thr Lys Phe Pro Val Trp Met Gly Ala Thr Thr Leu Phe Phe Gly  
405 410 415

Ala Ile Asn Gly Ala Lys Glu Met Leu Asp Val Ile Thr Glu Ile Asp  
420 425 430

Gly Lys Met Ile Thr Leu Ala Lys Val Thr Gly Asp Asp Asn Ala Leu  
435 440 445

Gln Gln Thr Phe Ile Asp Ala Asn Asn Ala Ala Ser Gln Phe Gly Gln  
450 455 460

Thr Leu Gly Ser Val Leu Asp Val Tyr Ala Glu Phe Ala Arg Gln Gly  
465 470 475 480

Val Lys Gly Asn Glu Leu Ser Gln Phe Ser Asn Ala Ala Leu Ile Ala  
485 490 495

Ala Asn Val Gly Glu Ile Asp Ala Lys Gln Ala Ser Glu Tyr Leu Thr  
500 505 510

Ser Met Ser Ala Gln Trp Glu Thr Thr Gly Asn Gln Ala Met Arg Gln  
515 520 525

Val Asp Ser Leu Asn Glu Val Ser Asn Lys Tyr Ala Thr Thr Val Glu  
530 535 540

Lys Leu Ala Gln Gly Gln Ala Lys Ala Gly Ser Thr Ala Lys Ser Met  
545 550 555 560

Gly Leu Thr Phe Asp Glu Thr Asn Gly Ile Ile Gly Ala Leu Thr Ala  
565 570 575

Lys Thr Lys Gln Ser Gly Asp Glu Ile Gly Asn Phe Met Lys Ala Thr  
580 585 590

Leu Pro Lys Leu Tyr Ser Gly Lys Gly Lys Ser Thr Ile Glu Gly Leu  
595 600 605

Gly Ile Ser Met Lys Asp Glu Asn Gly Gln Leu Lys Ser Ala Ile Ser  
610 615 620

Leu Leu Glu Glu Val Ser Gln Lys Thr Lys Asn Leu Glu Lys Asp Gln  
625 630 635 640

Lys Ala Ala Val Ile Asn Gly Leu Gly Gly Thr Tyr His Tyr Gln Arg  
645 650 655

Met Gln Val Leu Leu Asp Asp Leu Ser Lys Thr Asp Gly Leu Tyr Lys  
660 665 670

Gln Ile Lys Glu Ser Ser Glu Ser Ser Ala Gly Ser Ala Leu Gln Glu  
675 680 685

Asn Ala Lys Tyr Met Glu Ser Ile Glu Ala Lys Val Asn Gln Ala Lys  
690 695 700

Thr Ala Phe Glu Gln Phe Ala Leu Ala Val Gly Glu Thr Phe Ala Lys  
705 710 715 720

Ser Gly Met Leu Asp Gly Ile Arg Met Val Thr Gln Leu Leu Thr Gly  
725 730 735

Leu Thr His Gly Ile Thr Glu Leu Gly Thr Thr Ala Pro Ile Phe Gly  
740 745 750

Met Val Gly Gly Ala Ala Ser Leu Met Ser Lys Asn Val Arg Ser Gly  
755 760 765

Phe Glu Gly Ala Arg Ser Ser Val Ala Asn Tyr Ile Thr Glu Val Asn  
770 775 780

Lys Leu Ala Lys Val Asn Asn Ala Ala Gly Gln Val Val Gly Leu Gln  
785 790 795 800

Lys Val Gln Thr Gly Thr Ala Ser Gln Leu Gln Phe Asn Lys Asn Gly  
805 810 815

Glu Tyr Asp Lys Ala Ala Ser Gln Ala Lys Ala Ala Glu Gln Ala Thr  
820 825 830

Tyr Gln Phe Ser Lys Ala Gln Lys Asp Val Ser Ala Ser Ala Met Ile  
835 840 845

Ala Ser Gly Ala Ile Asn Lys Thr Thr Val Ala Thr Thr Ala Ser Thr  
850 855 860

Val Ala Thr Arg Ala Ala Thr Leu Ala Val Asn Gly Leu Lys Leu Ala  
865 870 875 880

Phe Arg Gly Leu Leu Ala Ala Thr Gly Val Gly Leu Ala Ile Thr Gly  
885 890 895

Val Ser Phe Val Leu Glu Lys Val Val Gly Ser Phe Asn Ala Ala Ser  
900 905 910

Gln Ala Ala Glu Gln Tyr Lys Gln Lys Gln Glu Gln Thr Lys Gln Ala  
915 920 925

Ile Ala Ser Met Ser Asn Gly Glu Ile Asn Ser Leu Ile Ser Ser Tyr  
930 935 940

Asp Lys Leu Gln Gln Lys Met Asn Ser Gly Ser Ala Phe Asn Thr Ala  
945 950 955 960

Glu Ala Glu Lys Tyr Lys Glu Val Thr Ser Gln Leu Ala Asn Ile Phe  
965 970 975

Pro Asp Leu Val Thr Gly Glu Asn Arg Tyr Gly Lys Glu Met Ala Gly  
980 985 990

Asn Lys Glu Val Met Lys Gln Lys Ile Glu Leu Ile Lys Gln Glu Met  
995 1000 1005

Glu Leu Glu Arg Gln Lys Asn Ala Ile Lys Gln Lys Glu Glu Gln  
1010 1015 1020

Asp Ala Tyr Ile Lys Glu Gln Asp Ser Leu Ala Lys Lys Asn Arg  
1025 1030 1035

Gly Gln Lys Trp Tyr Gln Leu Gly Gln Thr Pro Glu Leu Lys Leu  
1040 1045 1050

Gln Glu Gln Ala Arg Pro Thr Thr Val Ser Asp Asn Ser Asn Ile  
1055 1060 1065

Asn Lys Ile Asn Ala Thr Ile Gln Lys Val Lys Ser Gln Ala Gln  
1070 1075 1080

Ala Glu Lys Ala Leu Glu Gln Val Asp Lys Gln Leu Ala Gln Ser  
1085 1090 1095

Gln Thr Lys Asn Arg Gln Asn Glu Val Gln His Leu Gln Lys Val  
1100 1105 1110

Arg Gln Ala Leu Gln Asp Tyr Ile Thr Lys Thr Gly Gln Ala Asn  
1115 1120 1125

Gln Ala Thr Arg Ala Ala Val Leu Thr Ala Gln Gln Gln Phe Thr  
1130 1135 1140

Asn Gln Ile Ala Thr Met Lys Lys Leu Gly Thr Thr Gly Gln Gln  
1145 1150 1155

Val Met Thr Thr Ile Ser Asn Ser Val Ala Lys Thr Ala Lys Ser  
1160 1165 1170

Gly Lys Ala Ala Gln Ala Thr Phe Lys Ser Phe Glu Thr Ser Leu  
1175 1180 1185

Val Lys Ser Ser Ser Phe Lys Ser Lys Met Ala Ser Tyr Glu Ala  
1190 1195 1200

Ser Val Lys Lys Phe Lys Asn Ala Ala Asn Gln Ser Ala Lys Ile  
1205 1210 1215

Ala Ala Leu Lys Asp Val Glu Arg Asp Tyr Ser Lys Val Ala Lys  
1220 1225 1230

Gly Ile Met Gln Ala Ala Lys Ala Ala Asn Met Ser Lys Ser Gln  
1235 1240 1245

Met Lys Asp Leu Lys Ser Leu Gln Gln Asn Ile Gln Ala Glu  
1250 1255 1260

Thr Gly Phe Arg Ala Ser Val Ser Lys Ala Gly Lys Val Thr Ile  
1265 1270 1275

Asp Gln Ser Lys Lys Ile Lys Gln Asn Thr Ala Glu Thr Arg Arg  
1280 1285 1290

Asn Ser Ser Ala Lys Leu Gln Asn Ala Asp Ala Ser Asp Gln Ala  
1295 1300 1305

Ser Glu Glu Asn Lys Glu Leu Ala Asp Ser Met Arg Ala Gly Ile  
1310 1315 1320

Glu Ser Ser Gln Leu Leu Gly Lys Ala Met Gly Glu Leu Gln Ser  
1325 1330 1335

Gln Gly Thr Leu Ser Thr Glu Thr Leu Ile Glu Leu Thr Glu Lys

1340 1345 1350

Tyr Gly Asp Glu Ile Leu Ala Val Ala Gly Asp Gln Glu Ala Leu  
1355 1360 1365

Ser Asn Phe Ile Met Gln Lys Gln Asn Glu Glu Thr Asp Asn Tyr  
1370 1375 1380

Asn Lys Asn Leu Lys Thr Lys Leu Glu Asn Ser Ser Ser Tyr Tyr  
1385 1390 1395

Lys Ala Val Ala Gly Ala Asp Ser Ala Leu Ser Asn Tyr Leu Met  
1400 1405 1410

Glu Asn Tyr Gly Ile Asp Thr Lys Asn Tyr Lys Ser Leu Thr Glu  
1415 1420 1425

Val Lys Ala Lys Ile Thr Asp Leu Tyr Tyr Asn Gly Ser Ala Glu  
1430 1435 1440

Glu Gln Ala Lys Val Val Asp Ala Ile Ala Lys Ala Tyr His Ile  
1445 1450 1455

Asp Leu Ser Asn Tyr Gly Ser Leu Asn Glu Lys Lys Glu Ala Leu  
1460 1465 1470

Glu Asn Gln Leu Met Lys Ile Leu Gly Ser Lys Trp Lys Lys Tyr  
1475 1480 1485

Ile Gly Ser Val Ala Lys Asp Met Lys Ser Leu Gly Val Asp Ala  
1490 1495 1500

Gly Glu Val Gly Ala Asp Gly Phe Asp Asp Ser Lys Met Phe Asn  
1505 1510 1515

Pro Gly Ala Leu Ile Gly Ala Asn Asn Phe Gln Asn Val Ser Asn  
1520 1525 1530

Leu Ser Asn Ile Ser Asn Val Phe Asn Ser Leu Asn Gly Ala Phe  
1535 1540 1545

Asn Glu Ala Lys Asn Glu Ala Ala Gly Val Ser Arg Gly Leu Asp  
1550 1555 1560

Asp Ala Ala Ser Gly Leu Lys Asp Val Gly Asp Ser Ala Gly Ser  
1565 1570 1575

Ala Gly Ser Gly Leu Gly Lys Thr Ala Lys Gly Ala Asp Lys Ala  
1580 1585 1590

Ser Asp Ser Leu Asp Gly Thr Asn Lys Glu Leu Glu Lys Thr Lys  
1595 1600 1605

Glu Lys Ala Glu Glu Ala Gly Val Thr Val Lys Gln Leu Tyr Lys  
1610 1615 1620

Gln Phe Thr Val Thr Tyr Val Ala Asp Lys Leu Ser Met Ala  
1625 1630 1635

Leu Asp Lys Ile Asn Asn Lys Leu Glu Lys Gln Lys Leu Leu Thr  
1640 1645 1650

Glu Lys Tyr Ala Thr Trp Ser Ser Ser Tyr Arg Asn Ser Leu Lys  
1655 1660 1665

Ala Glu Asn Lys Leu Leu Asp Glu Lys Thr Ala Lys Ile Lys Lys  
1670 1675 1680

Gln Ile Glu Ser Met Lys Glu Gln Ile Ala Gln Gly Lys Val Ile  
1685 1690 1695

Glu Tyr Gly Leu Val Gly Lys Asp Ile Asn Val Pro Tyr Tyr Glu  
1700 1705 1710

Tyr Thr Ala Asn Asn Leu Asp Asp Gly Glu Thr Gly Arg Ile Ser  
1715 1720 1725

Arg Tyr Thr Gly Asn Ser Thr Gln Ala Lys Val Trp Asn Phe Phe  
1730 1735 1740

Lys Ser Lys Gly Leu Ser Asp His Ala Val Ala Gly Ile Met Gly  
1745 1750 1755

Asn Met Glu Arg Glu Ser Arg Phe Lys Pro Gly Ala Gln Glu Gln  
1760 1765 1770

Gly Gly Thr Gly Ile Gly Leu Val Gln Leu Ser Phe Gly Arg Ala  
1775 1780 1785

Asn Asn Leu Arg Asn Tyr Ala Ala Arg Arg Gly Lys Ser Trp Lys  
1790 1795 1800

Asp Leu Asn Thr Gln Leu Asp Phe Ile Trp Lys Glu Leu Asn Thr  
1805 1810 1815

Thr Glu Val Asn Ala Leu Arg Gly Leu Lys Ser Ala Thr Ser Val  
1820 1825 1830

Ile Gly Ala Ala Asn Ser Phe Gln Arg Leu Tyr Glu Arg Ala Gly  
1835 1840 1845

Val Val Ala Gln Gly Glu Arg Asn Ala Ala Ala Lys Lys Tyr Tyr  
1850 1855 1860

Arg Gln Phe Lys Gly Thr Asn Gly Ser Ser Gly Phe Leu Ser Gly  
1865 1870 1875

Gly Val Val Ala Gly Thr Asn Gly Lys Pro Leu Thr Ser Asp Arg  
1880 1885 1890

Asn Ala Tyr Ile Leu Asp Arg Gln Phe Gly Arg Tyr Asn Gly Gly  
1895 1900 1905

Gly Val His His Gly Arg Asp Ile Thr Ser Ala Thr Ile Asn Gly  
1910 1915 1920

Ser Pro Ile Lys Ala Ala Arg Ser Gly Ile Val Thr Phe Lys Gly  
1925 1930 1935

Trp Thr Gly Gly Gly Asn Thr Leu Ser Ile Phe Asp Gly Lys Asn  
1940 1945 1950

Thr Tyr Thr Tyr Met His Met Lys Asn Pro Ala Arg Val Val Lys  
1955 1960 1965

Gly Gln Arg Val Lys Ala Gly Gln Ile Val Gly Asn Val Gly Thr  
1970 1975 1980

Thr His Asp Arg Arg Leu Gly Gly Phe Ser Thr Gly Pro His Leu  
1985 1990 1995

His Val Gln Val Asn Leu Gly Lys Thr Pro Ser Gly Thr Phe Met  
2000 2005 2010

Asn Thr Phe Asn Gly Ala His Arg Ala Val Asp Pro Val Lys Tyr  
2015 2020 2025

Gly Tyr Thr Arg Val Ser Gly Gly Gly Ser Leu Asn Leu Gly Ser  
2030 2035 2040

Leu Thr Ser Gly His Ser Ala Met Ser Gly Ser Ile Ser Ala Ala  
2045 2050 2055

Met Ala Glu Asp Leu Asn Glu Ala Glu Gln Glu Arg Leu Asn Lys  
2060 2065 2070

Ile Glu Gln Ala Ile Asn Ala His Asn Lys Ala Glu Glu Met Lys  
2075 2080 2085

Gln Lys Val Asp Glu Leu Arg Lys Thr Leu Met Asp Lys Gln Leu  
2090 2095 2100

Glu Glu Val Gln Thr Ala Lys Glu Lys Ser Glu Asn Leu Tyr Asn  
2105 2110 2115

Ile Gln Lys Ser His Val Glu Glu Tyr Asp His Trp Arg Thr Leu  
2120 2125 2130

Gln Glu Ala Arg Ser Ala Lys Leu Glu Tyr Glu Leu Asn Lys Ile  
2135 2140 2145

Glu Phe Glu Lys Gly Arg Asn Thr Lys Glu Trp Arg Asn Lys Asn  
2150 2155 2160

Lys Gln Leu Gln Ala Ser Arg Gln Leu Glu Val Asn Phe Glu Asp  
2165 2170 2175

Ser Lys Ile Gln Tyr Ile Asn Lys Ala Leu Lys Lys Asn Ala Asn  
2180 2185 2190

Lys Ile Phe Gly Lys Asn Thr Val Asn Arg Asp Glu Phe Glu Thr  
2195 2200 2205

Met Lys Arg Asp Ala Gln Gln Asn Ile Arg Asp Leu Lys Ala Gly  
2210 2215 2220

Ile Gln Thr Ala Ser Gly Glu Ile Ala Thr Ser Met Ile Asp Gln  
2225 2230 2235

Ile Leu Asp Glu Tyr Glu Asp Arg Val Gly Lys Val Ser Ala Lys  
2240 2245 2250

Ile Glu Lys Met Gly Lys Gln Lys Glu Lys Leu Asp Leu Ala Asp

2255

2260

2265

Asn Lys Gln Ala Leu Lys Ser Ser Ser Leu Ser Arg Gln Gln Ala  
2270 2275 2280

Lys Asp Ser Lys Ser Leu Ala Ser Tyr Ile Asn Phe Tyr Ile Lys  
2285 2290 2295

Gln Leu Glu Arg Gln Leu Lys Leu Thr Gly Lys Asn His Glu Leu  
2300 2305 2310

Gln Gln Lys Val Lys Glu Gln Ile Lys Glu Met Lys Val Ala Tyr  
2315 2320 2325

Asp Asp Ala Thr Leu Ala Ala His Gln Tyr Ile Thr Glu Ala Ala  
2330 2335 2340

Glu Val Asp Thr Glu Arg Gln Leu Gln Leu Asn Ala Asn Arg Leu  
2345 2350 2355

Arg Asp Ala Gln Asn Glu Leu Ser Lys Ala Asp Tyr Lys Ala Gly  
2360 2365 2370

Phe Ile Ser Gln Glu Tyr Gln Ile Asp Leu Tyr Arg Lys Asn Gln  
2375 2380 2385

Glu Ala Lys Phe Lys Gly Tyr Leu Lys Glu Lys Glu Ala Leu Glu  
2390 2395 2400

Gln Asn Lys Ser Glu Leu Gln Asp Met Tyr Glu Ile Tyr Lys Ser  
2405 2410 2415

Val Pro Thr Gln Ala Gln Lys Ile Lys Glu Ala Leu Ile Glu Thr  
2420 2425 2430

Lys Asn Ala Ile Arg Asp Asn Asn Lys Gly Leu Tyr Asp Leu Lys  
2435 2440 2445

Tyr Asp Met Ala Asn Ser Val Ile Asn Gln Ile Lys Asp Ile Tyr  
2450 2455 2460

Ser Lys Gln Leu Glu Val Ala Thr Lys Ala Tyr Asp Asp Glu Tyr  
2465 2470 2475

Lys Ala Tyr Glu Lys Met Ile Asn Lys Lys Leu Lys Leu Ile Asp  
2480 2485 2490

Asp Glu Gln Thr Gln Glu Ser Phe Asn Lys Asp Val Arg Asp Arg  
2495 2500 2505

Thr Glu Ala Met Asp Lys Ile Arg Asp Glu Ile Ala Gln Arg Ser  
2510 2515 2520

Gly Asp Asp Ser Leu Ala Asn Gln Lys Lys Leu Lys Asp Leu Arg  
2525 2530 2535

Glu Gln Leu Lys Gln Gln Glu Glu Asp Tyr Thr Met Phe Ile Asn  
2540 2545 2550

Asn Lys Asn Arg Asp Asp Arg Arg Lys Ala Leu Gln Asp Glu Leu  
2555 2560 2565

Asn Asp Lys Asn Glu Gln Ile Gln Glu Gln Lys Glu Asp Leu Asn  
2570 2575 2580

Lys Ala Phe Gln Asp Leu Ile Gly Asp Thr Arg Arg Phe Asn Ala  
2585 2590 2595

Ile Gln Glu Ser Leu Met Glu Gly Gln Ile Asp Lys Tyr Lys Ser  
2600 2605 2610

Leu Ile Ala Asp Leu Thr Lys Tyr Val Asn Asp Asn Met Lys Glu  
2615 2620 2625

Ile Gly Arg Ser Thr Ser Glu Gly Ile Leu Asp Gly Leu Ala Ala  
2630 2635 2640

Ser Phe Lys Gly Leu Ser Ser Leu Ser Lys Glu Leu Gln Lys Gln  
2645 2650 2655

Glu Lys Asn Asn Leu Asn Pro Val Pro Asn Ser Lys Leu Lys Pro  
2660 2665 2670

Thr Lys Val Asp Glu Ala Thr Ile Ala Ala Ile Lys Lys Val Asn  
2675 2680 2685

Gly Leu Ser Pro Thr Thr Ile Leu Gln Gly Leu Asp Ile Lys Pro  
2690 2695 2700

Val Asn Leu Pro Lys Asp Val Lys Pro Ser Lys Thr Val Thr Asn  
2705 2710 2715

Asn Asn Lys Thr Thr Ala Lys Ala Leu Val Asn Ile Glu Asn Phe  
2720 2725 2730

Asn Gly Thr Lys Ala Glu Ala Asp Lys Leu Ala Asn Asn Leu Ala  
2735 2740 2745

Thr Ala Met Arg Lys Gln Gly Val Leu  
2750 2755

<210> 39  
<211> 319  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 39

Met Ala Glu Thr Lys Lys Gln Phe Glu Asn Lys Val Ser Val Thr Gly  
1 5 10 15

Thr Leu Lys Ser Leu Glu Val Thr Asp Leu Val Thr Ala Lys Lys Val  
20 25 30

Pro Met Lys Ile Ala Thr Leu Arg Ile Glu Thr Gly Lys Gly Glu Thr  
35 40 45

His Thr Ala Lys Met Met Ala Val Lys His Phe Glu Arg Asp Gly Val  
50 55 60

Lys Thr Glu Asn Lys Ser Tyr Ser Ala Ile Glu Thr Met Gln Lys Glu  
65 70 75 80

Tyr Val Ser Ile Glu Asp Ile Ser Glu Asn Lys Ala Gly Glu Asp Ala  
85 90 95

Glu Ala Thr Val Val Asn Val Asn Gly Ser Met Ser Ile Asn Met Tyr  
100 105 110

Lys Asn Lys Ala Glu Lys Val Val Glu Thr Asn Gln Ile Glu Ala Arg  
115 120 125

Phe Val Asn Arg Val Lys Asp Val Glu Asn Ala Gln Phe Gly Ala Glu  
130 135 140

Phe Thr Leu Gln Thr Tyr Leu Ile Ser Lys Gly Gln Arg Val Ile Lys  
145 150 155 160

Asn Glu Glu Glu Thr Asp Glu Val Thr Phe Lys Ala Ala Thr Ile Asp

165

170

175

Tyr Arg Gly Gln Ala His Pro Phe Glu Phe Thr Ala Asn Asp Glu Tyr  
180 185 190

Gly Val Ala Glu Trp Ile Glu Asp Glu Val Glu Leu Gly Gln Ser Leu  
195 200 205

Ile Leu Gln Gly Leu Ile Ile Asn Lys Phe Ile Val Glu Gln Val Glu  
210 215 220

Arg Ser Ser Ser Ala Gly Ile Gly Lys Ala Ile Val Asp Thr Arg Arg  
225 230 235 240

Glu Val Glu Arg Lys Leu Leu Val Glu Gly Ile Ile Pro Ile Glu Asp  
245 250 255

Glu Asp Asp Pro Lys Tyr Ile Thr Glu Glu Glu Ile Lys Glu Ala Asn  
260 265 270

Lys Lys Tyr Glu Asp Lys Lys Thr Glu Val Glu Ala Ser Thr Asn Gly  
275 280 285

Thr Lys Lys Thr Glu Val Lys Lys Gly Val Ala Thr Ser Lys Pro Lys  
290 295 300

Ala Ala Lys Pro Thr Ile Glu Ile Asp Asp Asp Asp Leu Pro Phe  
305 310 315

<210> 40  
<211> 797  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 40

Leu Pro Gln Ala Lys Lys Arg Thr Ser Thr Lys Arg Lys Gly Asn Lys  
1 5 10 15

Lys Thr Asn Lys Lys Gln Asn Glu Thr Pro Leu Arg Tyr Ile Phe  
20 25 30

Ser Ile Ile Val Val Ile Leu Ile Ile Leu Gly Ala Phe Gln Leu Gly  
35 40 45

Ile Ile Gly Arg Met Ile Asp Ser Phe Phe Asn Tyr Leu Phe Gly Met  
50 55 60

Ser Arg Tyr Leu Thr Tyr Ile Leu Val Leu Ile Ala Thr Ile Phe Ile  
 65 70 75 80

Thr Tyr Ser Lys Gln Ile Pro Arg Thr Arg Arg Ser Ile Gly Ala Ile  
 85 90 95

Val Leu Gln Leu Ala Leu Leu Phe Ile Ala Gln Leu Tyr Phe His Phe  
 100 105 110

Ser His Asn Ile Thr Ser Gln Arg Glu Pro Val Leu Ser Phe Val Tyr  
 115 120 125

Lys Ala Tyr Glu Gln Thr His Phe Pro Asn Phe Gly Gly Gly Leu Ile  
 130 135 140

Gly Phe Tyr Leu Leu Lys Leu Phe Ile Pro Leu Ile Ser Ile Val Gly  
 145 150 155 160

Val Ile Ile Ile Thr Ile Leu Leu Leu Ala Ser Ser Phe Ile Leu Leu  
 165 170 175

Leu Asn Leu Arg His Arg Asp Val Thr Lys Ser Leu Phe Asp Asn Leu  
 180 185 190

Lys Ser Ser Ser Asn His Ala Ser Glu Ser Ile Lys Gln Lys Arg Glu  
 195 200 205

Gln Asn Lys Ile Lys Lys Glu Glu Lys Ala Gln Leu Lys Glu Ala Lys  
 210 215 220

Ile Glu Arg Lys Lys Gln Lys Lys Ser Arg Gln Asn Asn Asn Val Ile  
 225 230 235 240

Lys Asp Val Ser Asp Phe Pro Glu Ile Ser Gln Ser Asp Asp Ile Pro  
 245 250 255

Ile Tyr Gly His Asn Glu Gln Glu Asp Lys Arg Pro Asn Thr Ala Asn  
 260 265 270

Gln Arg Gln Lys Arg Val Leu Asp Asn Glu Gln Phe Gln Gln Ser Leu  
 275 280 285

Pro Ser Thr Lys Asn Gln Ser Ile Asn Asn Asn Gln Pro Ser Thr Thr  
 290 295 300

Ala Glu Asn Asn Gln Gln Gln Ser Gln Ala Glu Gly Ser Ile Ser Glu  
305 310 315 320

Ala Gly Glu Glu Ala Asn Ile Glu Tyr Thr Val Pro Pro Leu Ser Leu  
325 330 335

Leu Lys Gln Pro Thr Lys Gln Lys Thr Thr Ser Lys Ala Glu Val Gln  
340 345 350

Arg Lys Gly Gln Val Leu Glu Ser Thr Leu Lys Asn Phe Gly Val Asn  
355 360 365

Ala Lys Val Thr Gln Ile Lys Ile Gly Pro Ala Val Thr Gln Tyr Glu  
370 375 380

Ile Gln Pro Ala Gln Gly Val Lys Val Ser Lys Ile Val Asn Leu His  
385 390 395 400

Asn Asp Ile Ala Leu Ala Ala Lys Asp Val Arg Ile Glu Ala  
405 410 415

Pro Ile Pro Gly Arg Ser Ala Val Gly Ile Glu Val Pro Asn Asp Lys  
420 425 430

Ile Ser Leu Val Thr Leu Lys Glu Val Leu Glu Asp Lys Phe Pro Ser  
435 440 445

Lys Tyr Lys Leu Glu Val Gly Ile Gly Arg Asp Ile Ser Gly Asp Pro  
450 455 460

Ile Ser Ile Gln Leu Asn Glu Met Pro His Leu Leu Val Ala Gly Ser  
465 470 475 480

Thr Gly Ser Gly Lys Ser Val Cys Ile Asn Gly Ile Ile Thr Ser Ile  
485 490 495

Leu Leu Asn Thr Lys Pro His Glu Val Lys Leu Met Leu Ile Asp Pro  
500 505 510

Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ile  
515 520 525

Pro Val Val Thr Asn Pro His Lys Ala Ser Gln Ala Leu Glu Lys Ile  
530 535 540

Val Ser Glu Met Glu Arg Arg Tyr Asp Leu Phe Gln His Ser Ser Thr

545

550

555

560

Arg Asn Ile Glu Gly Tyr Asn Gln Tyr Ile Arg Lys Gln Asn Glu Glu  
565 570 575

Leu Asp Glu Lys Gln Pro Glu Leu Pro Tyr Ile Val Val Ile Val Asp  
580 585 590

Glu Leu Ala Asp Leu Met Met Val Ala Gly Lys Glu Val Glu Asn Ala  
595 600 605

Ile Gln Arg Ile Thr Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile  
610 615 620

Val Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Ile Ile Lys  
625 630 635 640

Asn Asn Ile Pro Ser Arg Ile Ala Phe Ala Val Ser Ser Gln Thr Asp  
645 650 655

Ser Arg Thr Ile Ile Gly Ala Gly Gly Ala Glu Lys Leu Leu Gly Lys  
660 665 670

Gly Asp Met Leu Tyr Val Gly Asn Gly Glu Ser Thr Thr Thr Arg Ile  
675 680 685

Gln Gly Ala Phe Leu Ser Asp Gln Glu Val Gln Asp Val Val Asn Tyr  
690 695 700

Val Val Glu Gln Gln Lys Ala Asn Tyr Val Lys Glu Met Glu Pro Asp  
705 710 715 720

Ala Pro Val Asp Lys Ser Glu Met Lys Ser Glu Asp Ala Leu Tyr Asp  
725 730 735

Glu Ala Tyr Leu Phe Val Ile Glu Lys Gln Lys Ala Ser Thr Ser Leu  
740 745 750

Leu Gln Arg Gln Phe Arg Ile Gly Tyr Asn Arg Ala Ser Arg Leu Met  
755 760 765

Asp Asp Leu Glu Arg Asn Gln Val Ile Gly Pro Gln Lys Gly Ser Lys  
770 775 780

Pro Arg Gln Ile Leu Val Asp Leu Glu Asn Asp Glu Val  
785 790 795

<210> 41

<211> 429

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 41

Met Lys Thr His Gln Tyr Glu Leu Ile Asp Glu Lys Val Phe Glu His  
1 5 10 15

Glu Phe Asp Asn Gly Leu Lys Leu Phe Ile Ile Pro Lys Pro Gly Phe  
20 25 30

Gln Lys Thr Tyr Val Thr Tyr Thr Gln Phe Gly Ser Leu Asp Asn  
35 40 45

His Phe Lys Pro Ile Gly Ser Gln Gln Phe Val Lys Val Pro Asp Gly  
50 55 60

Val Ala His Phe Leu Glu His Lys Leu Phe Glu Lys Glu Asp Glu Asp  
65 70 75 80

Leu Phe Thr Ala Phe Ala Glu Glu Asn Ala Gln Ala Asn Ala Phe Thr  
85 90 95

Ser Phe Asp Arg Thr Ser Tyr Leu Phe Ser Ala Thr Ser Asn Ile Glu  
100 105 110

Ser Asn Ile Lys Arg Leu Leu Asn Met Val Glu Thr Pro Tyr Phe Thr  
115 120 125

Glu Glu Thr Val Asn Lys Glu Lys Gly Ile Ile Ala Glu Glu Ile Lys  
130 135 140

Met Tyr Gln Glu Gln Pro Gly Tyr Lys Leu Met Phe Asn Thr Leu Arg  
145 150 155 160

Ala Met Tyr Ser Lys His Pro Ile Arg Val Asp Ile Ala Gly Ser Val  
165 170 175

Glu Ser Ile Tyr Glu Ile Thr Lys Asp Asp Leu Tyr Leu Cys Tyr Glu  
180 185 190

Thr Phe Tyr His Pro Ser Asn Met Val Leu Phe Val Val Gly Asp Val  
195 200 205

Ser Pro Gln Ser Ile Ile Lys Leu Val Glu Lys His Glu Asn Gln Arg  
210 215 220

Asn Lys Thr Tyr Gln Pro Arg Ile Glu Arg Ala Gln Ile Asp Glu Pro  
225 230 235 240

Arg Glu Ile Asn Gln Arg Phe Val Ser Glu Lys Met Lys Leu Gln Ser  
245 250 255

Pro Arg Leu Met Leu Gly Phe Lys Asn Glu Pro Leu Asp Glu Ser Ala  
260 265 270

Thr Lys Phe Val Gln Arg Asp Leu Glu Met Thr Phe Phe Tyr Glu Leu  
275 280 285

Val Phe Gly Glu Glu Thr Glu Phe Tyr Gln Gln Leu Leu Asn Lys Asp  
290 295 300

Leu Ile Asp Glu Thr Phe Gly Tyr Gln Phe Val Leu Glu Pro Ser Tyr  
305 310 315 320

Ser Phe Ser Ile Ile Thr Ser Ala Thr Gln Gln Pro Asp Leu Phe Lys  
325 330 335

Gln Leu Ile Met Asp Glu Leu Arg Lys Tyr Lys Gly Asn Leu Lys Asp  
340 345 350

Gln Glu Ala Phe Asp Leu Leu Lys Lys Gln Phe Ile Gly Glu Phe Ile  
355 360 365

Ser Ser Leu Asn Ser Pro Glu Tyr Ile Ala Asn Gln Tyr Ala Lys Leu  
370 375 380

Tyr Phe Glu Gly Val Ser Val Phe Asp Met Leu Asp Ile Val Glu Asn  
385 390 395 400

Ile Thr Leu Glu Ser Val Asn Glu Thr Ser Glu Leu Phe Leu Asn Phe  
405 410 415

Asp Gln Leu Val Asp Ser Arg Leu Glu Met Glu Asn Arg  
420 425

<210> 42  
<211> 329  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 42

Met Thr Glu Gln Lys Asp Ile Lys Glu Thr Glu Tyr Arg Arg Gln Lys  
1 5 10 15

Gly Thr Thr Ser Thr Pro Ser Arg Arg Arg Asn Lys Lys Arg Met Arg  
20 25 30

Lys Leu Pro Phe Ile Ile Leu Val Ile Leu Ile Ile Leu Ile Ser Ile  
35 40 45

Ile Val Tyr Ile Thr His Gln Tyr Asn Ser Gly Met Lys Tyr Ala Lys  
50 55 60

Glu His Ala Lys Asp Val Lys Val His Lys Phe Asn Gly Asn Met Lys  
65 70 75 80

Asn Asp Gly Lys Ile Ser Val Leu Val Leu Gly Ala Asp Lys Ala Gln  
85 90 95

Gly Gly Lys Ser Arg Thr Asp Ser Ile Met Ile Val Gln Tyr Asp Tyr  
100 105 110

Val His Lys Lys Met Lys Met Met Ser Val Met Arg Asp Ile Tyr Ala  
115 120 125

Asp Ile Pro Gly Tyr Asp Lys Tyr Lys Ile Asn Ala Ala Tyr Ser Leu  
130 135 140

Gly Gly Pro Glu Leu Leu Arg Lys Thr Leu Asn Lys Asn Leu Gly Val  
145 150 155 160

Asn Pro Glu Tyr Tyr Ala Val Val Asp Phe Thr Gly Phe Glu Lys Met  
165 170 175

Ile Asp Glu Leu Gln Pro Asn Gly Val Pro Ile Asp Val Glu Lys Asp  
180 185 190

Met Ser Glu Asn Ile Gly Val Ser Leu Lys Lys Gly His His Lys Leu  
195 200 205

Asn Gly Lys Glu Leu Leu Gly Tyr Ala Arg Phe Arg His Asp Pro Glu  
210 215 220

Gly Asp Phe Gly Arg Val Arg Arg Gln Gln Gln Val Met Gln Thr Leu  
225 230 235 240

Lys Gln Glu Leu Val Asn Phe Asn Thr Val Ala Lys Leu Pro Lys Val  
245 250 255

Ala Gly Ile Leu Arg Gly Tyr Val Asn Thr Asn Met Pro Asn Ser Ala  
260 265 270

Ile Phe Gln Thr Gly Ile Ser Phe Gly Ile Arg Gly Asp Lys Asp Val  
275 280 285

Gln Ser Leu Thr Val Pro Ile Lys Gly Ser Tyr Gln Asp Ile Asn Thr  
290 295 300

Asn Asn Asp Gly Ser Ala Leu Gln Ile Asp Ser Glu Lys Asn Lys Gln  
305 310 315 320

Ala Ile Lys Asn Phe Phe Glu Asp Asn  
325

<210> 43  
<211> 627  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 43

Met Glu Ala Tyr Lys Ile Glu His Leu Asn Lys Ser Tyr Ala Asp Lys  
1 5 10 15

Glu Ile Phe Asn Asp Leu Asn Leu Ser Ile Ser Glu His Glu Arg Ile  
20 25 30

Gly Leu Val Gly Ile Asn Gly Thr Gly Lys Ser Thr Leu Leu Lys Val  
35 40 45

Ile Gly Gly Leu Asp Glu Asp Phe Thr Ala Asp Ile Thr His Pro Asn  
50 55 60

Gln Tyr Arg Ile Arg Tyr Ser Ser Gln Lys Gln Asp Leu Asn Gly His  
65 70 75 80

Met Thr Val Phe Glu Ala Val Leu Ser Ser Asp Thr Pro Thr Leu Arg  
85 90 95

Ile Ile Lys Lys Tyr Glu Glu Ala Val Asn Arg Tyr Ala Leu Asp Gln  
100 105 110

Ser Asp Ser Asn Phe Asn Lys Met Met Glu Ala Gln Glu Glu Met Asp

115

120

125

Gln Lys Asp Ala Trp Asp Tyr Asn Ala Glu Ile Lys Thr Ile Leu Ser  
130 135 140

Lys Leu Gly Ile His Asp Thr Thr Lys Lys Ile Val Glu Leu Ser Gly  
145 150 155 160

Gly Gln Gln Lys Arg Val Val Leu Ala Lys Thr Leu Ile Glu Gln Pro  
165 170 175

Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Phe Glu Ser  
180 185 190

Ile Arg Trp Leu Ile Asn Tyr Val Lys Gln Tyr Pro His Thr Val Leu  
195 200 205

Phe Val Thr His Asp Arg Tyr Phe Leu Asn Glu Val Ser Thr Arg Ile  
210 215 220

Ile Glu Leu Asp Arg Gly Lys Leu Lys Thr Tyr Pro Gly Asn Tyr Glu  
225 230 235 240

Asp Tyr Ile Val Met Arg Ala Glu Asn Glu Leu Val Glu Gln Lys Gln  
245 250 255

Gln Glu Lys Gln Lys Ala Leu Tyr Lys Gln Glu Leu Ala Trp Met Arg  
260 265 270

Ala Gly Ala Lys Ala Arg Thr Thr Lys Gln Gln Ala Arg Ile Asn Arg  
275 280 285

Phe Asn Gln Leu Glu Ser Asp Val Lys Thr Gln His Thr Gln Asp Lys  
290 295 300

Gly Glu Leu Asn Leu Ala Tyr Ser Arg Leu Gly Lys Gln Val Tyr Glu  
305 310 315 320

Leu Lys Asn Leu Ser Lys Ser Ile Asn Asn Lys Val Leu Phe Glu Asp  
325 330 335

Val Thr Glu Ile Ile Gln Ser Gly Arg Arg Ile Gly Ile Val Gly Pro  
340 345 350

Asn Gly Ala Gly Lys Thr Thr Leu Leu Asn Ile Leu Ser Asn Glu Asp  
355 360 365

Gln Asp Tyr Glu Gly Glu Leu Lys Ile Gly Gln Thr Val Lys Val Ala  
370 375 380

Tyr Phe Lys Gln Thr Glu Lys Thr Leu Asp Arg Asp Ile Arg Val Ile  
385 390 395 400

Asp Tyr Leu Arg Glu Glu Ser Glu Met Ala Lys Glu Lys Asp Gly Thr  
405 410 415

Ser Ile Ser Val Thr Gln Leu Leu Glu Arg Phe Leu Phe Pro Ser Ala  
420 425 430

Thr His Gly Lys Lys Val Tyr Lys Leu Ser Gly Gly Glu Gln Lys Arg  
435 440 445

Leu Tyr Leu Leu Arg Leu Leu Val His Lys Pro Asn Val Leu Leu Leu  
450 455 460

Asp Glu Pro Thr Asn Asp Leu Asp Thr Glu Thr Leu Thr Ile Leu Glu  
465 470 475 480

Asp Tyr Ile Asp Asp Phe Gly Gly Ser Val Ile Thr Val Ser His Asp  
485 490 495

Arg Tyr Phe Leu Asn Lys Val Val Gln Glu Tyr Trp Phe Ile His Asp  
500 505 510

Gly Lys Ile Glu Lys Ile Ile Gly Ser Phe Glu Asp Tyr Glu Ser Phe  
515 520 525

Lys Lys Glu His Glu Arg Gln Ala Met Leu Ser Lys Gln Thr Glu Gln  
530 535 540

Gln Asn Lys His Lys His Gln Pro Lys Lys Thr Gly Leu Ser Tyr  
545 550 555 560

Lys Glu Lys Leu Glu Tyr Glu Thr Ile Met Thr Arg Ile Glu Met Thr  
565 570 575

Glu Thr Arg Leu Glu Asp Leu Glu Gln Glu Met Ile Asn Ala Ser Asp  
580 585 590

Asn Tyr Ala Arg Ile Lys Glu Leu Asn Glu Glu Lys Glu Gln Leu Glu  
595 600 605

Ala Thr Tyr Glu Ala Asp Ile Thr Arg Trp Ser Glu Leu Glu Glu Ile  
610 615 620

Lys Glu Gln  
625

<210> 44  
<211> 270  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 44

Met Lys Leu Phe Gly Ile Ile Leu Val Leu Ala Leu Thr Ile Ala  
1 5 10 15

Leu Ala Ala Cys Gly Gly Lys Asp Lys Glu Lys Thr Ile Thr Val  
20 25 30

Gly Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys Ala Lys Pro  
35 40 45

Leu Leu Lys Lys Gly Tyr Asp Leu Lys Ile Lys Pro Ile Asn Asp  
50 55 60

Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile Asp Ala Asn  
65 70 75 80

Phe Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Ser Lys Glu Lys Gly  
85 90 95

Tyr Lys Ile Glu Ser Ala Gly Asn Val Glu Leu Glu Pro Met Ala Val  
100 105 110

Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Asp Leu Pro Lys Gly Ala Thr  
115 120 125

Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe Leu Lys Phe  
130 135 140

Phe Val Asp Glu Gly Leu Ile Lys Leu Lys Lys Gly Val Lys Ile Glu  
145 150 155 160

Asn Ala Lys Phe Asp Asp Ile Thr Glu Asn Lys Lys Asp Ile Lys Phe  
165 170 175

Asn Asn Lys Gln Ser Ala Glu Tyr Leu Pro Lys Ile Tyr Gln Asn Gln

180

185

190

Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Tyr Ala Ile Asp Gln Lys  
195 200 205

Leu Ser Pro Lys Lys Asp Ser Ile Ala Leu Glu Ser Pro Lys Asp Asn  
210 215 220

Pro Tyr Ala Asn Leu Ile Ala Val Lys Lys Gly His Lys Asp Asp Lys  
225 230 235 240

Asn Ile Lys Val Leu Met Glu Val Leu Gln Ser Lys Glu Ile Gln Asp  
245 250 255

Tyr Ile Lys Asp Lys Tyr Asp Gly Ala Val Val Pro Ala Lys  
260 265 270

<210> 45  
<211> 439  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 45

Met Glu Leu Thr Ile Tyr His Thr Asn Asp Ile His Ser His Leu Asn  
1 5 10 15

Glu Tyr Ala Arg Ile Gln Ala Tyr Met Ala Lys His Arg Pro Gln Leu  
20 25 30

Glu His Pro Ser Leu Tyr Ile Asp Ile Gly Asp His Val Asp Leu Ser  
35 40 45

Ala Pro Val Thr Glu Ala Thr Val Gly His Lys Asn Ile Glu Leu Leu  
50 55 60

Asn Glu Ala His Cys Asp Ile Ala Thr Ile Gly Asn Asn Glu Gly Met  
65 70 75 80

Thr Ile Ser His Asp Ala Leu Gln Asn Leu Tyr Asn Asp Ala Asp Phe  
85 90 95

Lys Val Ile Cys Thr Asn Val Ile Asp Glu Glu Gly His Leu Pro His  
100 105 110

His Ile Thr Ser Ser Tyr Ile Lys Glu Ile Lys Gly Thr Arg Ile Leu  
115 120 125

Phe Val Ala Ala Thr Ala Pro Phe Thr Pro Phe Tyr Arg Ala Leu Asp  
130 135 140

Trp Ile Val Thr Asp Pro Leu Ala Ala Ile Lys Asp Glu Ile Asn Ala  
145 150 155 160

His Gln Gly Glu Tyr Asp Leu Leu Met Val Met Ser His Val Gly Ile  
165 170 175

Phe Phe Asp Glu Lys Leu Cys Gln Glu Ile Pro Glu Ile Asp Val Ile  
180 185 190

Phe Gly Ser His Thr His His Phe Glu His Gly Glu Ile Asn Asn  
195 200 205

Gly Val Leu Met Ala Ala Ala Gly Lys Tyr Gly Tyr Tyr Leu Gly Glu  
210 215 220

Val Asn Ile Thr Ile Glu Asn Gly Lys Ile Val Asp Lys Ile Ala Lys  
225 230 235 240

Ile His Pro Ile Glu Thr Leu Pro Leu Val Glu Thr His Phe Glu Glu  
245 250 255

Glu Gly Arg Ala Leu Leu Ser Lys Pro Val Val Asn His His Val Asn  
260 265 270

Leu Val Lys Arg Thr Asp Val Val Thr Arg Thr Ser Tyr Leu Leu Ala  
275 280 285

Glu Ser Val Tyr Glu Phe Ser Arg Ala Asp Cys Ala Ile Val Asn Ala  
290 295 300

Gly Leu Ile Val Asn Gly Ile Glu Ala Asp Lys Val Thr Glu Tyr Asp  
305 310 315 320

Ile His Arg Met Leu Pro His Pro Ile Asn Ile Val Arg Val Arg Leu  
325 330 335

Thr Gly Lys Gln Leu Lys Gln Val Ile Gln Lys Ser Gln Lys Gln Glu  
340 345 350

Tyr Met His Glu His Ala Gln Gly Leu Gly Phe Arg Gly Asp Ile Phe  
355 360 365

Gly Gly Tyr Ile Leu Tyr Asn Leu Gly Phe Ile Glu Ser Glu Asp Arg  
370 375 380

Tyr Phe Ile Gly Asp Glu Glu Ile Gln Asn Asp Lys Gln Tyr Thr Leu  
385 390 395 400

Gly Thr Val Asp Met Tyr Thr Phe Gly Arg Tyr Phe Pro Leu Leu Lys  
405 410 415

Gly Leu Ser Thr Asp Tyr Ile Met Pro Glu Phe Leu Arg Asp Ile Phe  
420 425 430

Lys Glu Lys Leu Leu Lys Leu  
435

<210> 46  
<211> 203  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 46

Met Glu Lys Val Ile Tyr Leu Ala Gly His Ile Leu Asn Glu Ala Met  
1 5 10 15

Val Asp Tyr Arg Glu Lys Gln His Asn Gln Val Glu Ala Ile Glu Gly  
20 25 30

Val Lys Pro Tyr Ser Pro His Gln Asp Lys Ser Ile Asn Asp Lys Ser  
35 40 45

Asn Ala Val Gln Glu Gly Leu Ala Glu Arg Ile Leu Lys Asn Asp Phe  
50 55 60

Thr Ala Met Glu Lys Ser Asp Ile Tyr Val Leu Asp Val Leu Asn Glu  
65 70 75 80

Gly Leu Gly Thr Ile Ser Glu Leu Gly Ile Ile Ile Gly Met Lys Lys  
85 90 95

Gln Ala Gln Lys Thr Ile Asp Arg Leu Ser Val Leu Ser Glu Glu Ile  
100 105 110

Lys His Asp Val Tyr Gly Asp Gln Thr Glu Ala Tyr Asp Leu Ile Gln  
115 120 125

Asp Glu Ile Tyr Lys Gln Glu Lys Ile Leu Asn Lys Thr Val Leu Cys  
130 135 140

Tyr Cys Ser Asp Ile Arg Gln Gly His Gly Lys Pro Tyr Thr Asp Pro  
145 150 155 160

Asp Arg Ala Glu Phe Ser Thr Asn Gln Phe Val Tyr Gly Met Val Leu  
165 170 175

Glu Ala Thr Asn Gly Glu Gly Phe Ile Thr Trp Asp Gln Val Leu His  
180 185 190

Arg Leu Asp Leu Phe Gly Ser Gly Leu Ile Val  
195 200

<210> 47

<211> 59

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 47

Met Ser Lys Lys Phe Arg Val Glu Asp Lys Glu Thr Ile Ala Asp Cys  
1 5 10 15

Leu Asp Arg Met Lys Lys Glu Gly Phe Met Pro Ile Arg Arg Ile Glu  
20 25 30

Lys Pro Val Tyr Lys Glu Asn Lys Asp Gly Ser Ile Glu Ile Leu Lys  
35 40 45

Gln Asp Ile Ile Phe Val Gly Ala Leu Ile Gln  
50 55

<210> 48

<211> 3692

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 48

Met Asn Leu Phe Arg Lys Gln Lys Phe Ser Ile Arg Lys Phe Asn Ile  
1 5 10 15

Gly Ile Phe Ser Ala Leu Ile Ala Thr Val Ala Phe Leu Ala His Pro  
20 25 30

Gly Gln Ala Thr Ala Ser Glu Leu Glu Pro Ser Gln Asn Asn Asp Thr  
35 40 45

Thr Ala Gln Ser Asp Gly Gly Leu Glu Asn Thr Ser Gln Ser Asn Pro

50

55

60

Ile Ser Glu Glu Thr Thr Asn Thr Leu Ser Gly Gln Thr Val Pro Ser  
 65 70 75 80

Ser Thr Glu Asn Lys Gln Thr Gln Asn Val Pro Asn His Asn Ala Gln  
 85 90 95

Pro Ile Ala Ile Asn Thr Glu Glu Ala Glu Ser Ala Gln Thr Ala Ser  
 100 105 110

Tyr Thr Asn Ile Asn Glu Asn Asn Asp Thr Ser Asp Asp Gly Leu His  
 115 120 125

Val Asn Gln Pro Ala Lys His His Ile Glu Ala Gln Ser Glu Asp Val  
 130 135 140

Thr Asn His Thr Asn Ser Asn His Ser Asn Ser Ser Ile Pro Glu Asn  
 145 150 155 160

Lys Ala Thr Thr Glu Ser Ser Lys Pro Lys Lys Arg Gly Lys Arg  
 165 170 175

Ser Leu Asp Thr Asn Asn Gly Asn Asp Thr Thr Ser Thr Thr Gln Asn  
 180 185 190

Thr Asp Pro Asn Leu Ser Asn Thr Gly Pro Asn Gly Ile Asn Thr Val  
 195 200 205

Ile Thr Phe Asp Asp Leu Gly Ile Lys Thr Ser Thr Asn Arg Ser Arg  
 210 215 220

Pro Glu Val Lys Val Val Asp Ser Leu Asn Gly Phe Thr Met Val Asn  
 225 230 235 240

Gly Gly Lys Val Gly Leu Leu Asn Ser Val Leu Glu Arg Thr Ser Val  
 245 250 255

Phe Asp Ser Ala Asp Pro Lys Asn Tyr Gln Ala Ile Asp Asn Val Val  
 260 265 270

Ala Leu Gly Arg Ile Lys Gly Asn Asp Pro Asn Asp His Asp Gly Phe  
 275 280 285

Asn Gly Ile Glu Lys Glu Phe Ser Val Asn Pro Asn Ser Glu Ile Ile  
 290 295 300

Phe Ser Phe Asn Thr Met Thr Ala Lys Asn Arg Lys Gly Gly Thr Gln  
305 310 315 320

Leu Val Leu Arg Asn Ala Glu Asn Asn Gln Glu Ile Ala Ser Thr Asp  
325 330 335

Ile Gln Gly Gly Val Tyr Arg Leu Phe Lys Leu Pro Asp Asn Val  
340 345 350

His Arg Leu Lys Val Gln Phe Leu Pro Met Asn Glu Ile His Ser Asp  
355 360 365

Phe Lys Arg Ile Gln Gln Leu His Asp Gly Tyr Arg Tyr Tyr Ser Phe  
370 375 380

Ile Asp Thr Ile Gly Val Asn Ser Gly Ser His Leu Tyr Val Lys Ser  
385 390 395 400

Arg Gln Val Asn Lys Asn Val Lys Asn Gly Lys Glu Phe Glu Val Asn  
405 410 415

Thr Arg Ile Glu Asn Asn Gly Asn Phe Ala Ala Ala Ile Gly Gln Asn  
420 425 430

Glu Leu Thr Tyr Lys Val Thr Leu Pro Glu Asn Phe Glu Tyr Val Asp  
435 440 445

Asn Ser Thr Glu Val Ser Phe Val Asn Gly Asn Val Pro Asn Ser Thr  
450 455 460

Val Asn Pro Phe Ser Val Asn Phe Asp Arg Gln Asn His Thr Leu Thr  
465 470 475 480

Phe Ser Ser Asn Gly Leu Asn Leu Gly Arg Ser Ala Gln Asp Val Ala  
485 490 495

Arg Phe Leu Pro Asn Lys Ile Leu Asn Ile Arg Tyr Lys Leu Arg Pro  
500 505 510

Val Asn Ile Ser Thr Pro Arg Glu Val Thr Phe Asn Glu Ala Ile Lys  
515 520 525

Tyr Lys Thr Phe Ser Glu Tyr Tyr Ile Asn Thr Asn Asp Asn Thr Val  
530 535 540

Thr Gly Gln Gln Thr Pro Phe Ser Ile Asn Val Ile Met Asn Lys Asp  
545 550 555 560

Asp Leu Ser Glu Gln Val Asn Lys Asp Ile Ile Pro Ser Asn Tyr Thr  
565 570 575

Leu Ala Ser Tyr Asn Lys Tyr Asn Lys Leu Lys Glu Arg Ala Gln Thr  
580 585 590

Val Leu Asp Glu Glu Thr Asn Asn Thr Pro Phe Asn Gln Arg Tyr Ser  
595 600 605

Gln Thr Gln Ile Asp Asp Leu Leu His Glu Leu Gln Thr Thr Leu Ile  
610 615 620

Asn Arg Val Ser Ala Ser Arg Glu Ile Asn Asp Lys Ala Gln Glu Met  
625 630 635 640

Thr Asp Ala Val Tyr Asp Ser Thr Glu Leu Thr Thr Glu Glu Lys Asp  
645 650 655

Thr Leu Val Asp Gln Ile Glu Asn His Lys Asn Glu Ile Ser Asn Asn  
660 665 670

Ile Asp Asp Glu Leu Thr Asp Asp Gly Val Glu Arg Val Lys Glu Ala  
675 680 685

Gly Leu His Thr Leu Glu Ser Asp Thr Pro His Pro Val Thr Lys Pro  
690 695 700

Asn Ala Arg Gln Val Val Asn Asn Arg Ala Asp Gln Gln Lys Thr Leu  
705 710 715 720

Ile Arg Asn Asn His Glu Ala Thr Thr Glu Glu Gln Asn Glu Ala Ile  
725 730 735

Arg Gln Val Glu Ala His Ser Ser Asp Ala Ile Ala Lys Ile Gly Glu  
740 745 750

Ala Glu Thr Asp Thr Thr Val Asn Glu Ala Arg Asp Asn Gly Thr Lys  
755 760 765

Leu Ile Ala Thr Asp Val Pro Asn Pro Thr Lys Lys Ala Glu Ala Arg  
770 775 780

Ala Ala Val Thr Asn Ser Ala Asn Ser Lys Ile Lys Asp Ile Asn Asn  
785 790 795 800

Asn Thr Gln Ala Thr Leu Asp Glu Arg Asn Asp Ala Ile Ala Leu Val  
805 810 815

Asn Arg Ser Lys Asp Glu Ala Ile Gln Asn Ile Asn Thr Ala Gln Gly  
820 825 830

Asn Asp Asp Val Thr Glu Ala Gln Asn Asn Gly Thr Asn Thr Ile Gln  
835 840 845

Gln Val Pro Leu Thr Pro Val Lys Arg Gln Asn Ala Ile Ala Thr Ile  
850 855 860

Asn Ala Lys Ala Asp Glu Gln Lys Arg Leu Ile Gln Ala Asn Asn Asn  
865 870 875 880

Ala Thr Thr Glu Glu Lys Ala Asp Ala Glu Arg Lys Val Asn Glu Ala  
885 890 895

Val Ile Thr Ala Asn Gln Asn Ile Thr Asn Ala Thr Thr Asn Arg Asp  
900 905 910

Val Asp Gln Ala Gln Thr Thr Gly Ser Gly Ile Ile Ser Ala Ile Ser  
915 920 925

Pro Ala Thr Lys Ile Lys Glu Asp Ala Arg Ala Ala Val Glu Ala Lys  
930 935 940

Ala Ile Ala Gln Asn Gln Ile Asn Ser Asn Asn Met Ala Thr Thr  
945 950 955 960

Glu Glu Lys Glu Asp Ala Leu Asn Gln Val Glu Ala His Lys Gln Ala  
965 970 975

Ala Ile Ala Thr Ile Asn Gln Ala Gln Ser Thr Gln Gln Val Ser Glu  
980 985 990

Ala Lys Asn Asn Gly Ile Asn Thr Ile Asn Gln Asp Gln Pro Asn Ala  
995 1000 1005

Val Lys Lys Asn Asn Thr Lys Ile Ile Leu Glu Gln Lys Gly Asn  
1010 1015 1020

Glu Lys Lys Ser Ala Ile Ala Gln Thr Pro Asp Ala Thr Thr Glu

1025 1030 1035

Glu Lys Gln Glu Ala Val Ser Ala Val Ser Gln Ala Val Thr Asn  
1040 1045 1050

Gly Ile Thr His Ile Asn Gln Ala Asn Ser Asn Asp Asp Val Asp  
1055 1060 1065

Gln Glu Leu Ser Asn Ala Glu Gln Ile Ile Thr Gln Thr Asn Val  
1070 1075 1080

Asn Val Gln Lys Lys Pro Gln Ala Arg Gln Ala Leu Ile Ala Lys  
1085 1090 1095

Thr Asn Glu Arg Gln Ser Thr Ile Asn Thr Asp Asn Glu Gly Thr  
1100 1105 1110

Ile Glu Glu Lys Gln Lys Ala Ile Gln Ser Leu Asn Asp Ala Lys  
1115 1120 1125

Asn Leu Ala Asp Glu Gln Ile Thr Gln Ala Ala Ser Asn Gln Asn  
1130 1135 1140

Val Asp Asn Ala Leu Asn Ile Gly Ile Ser Asn Ile Ser Lys Ile  
1145 1150 1155

Gln Thr Asn Phe Thr Lys Lys Gln Gln Ala Arg Asp Gln Val Asn  
1160 1165 1170

Gln Lys Phe Gln Glu Lys Glu Ala Glu Leu Asn Ser Thr Pro His  
1175 1180 1185

Ala Thr Gln Asp Glu Lys Gln Asp Ala Leu Thr Arg Leu Thr Gln  
1190 1195 1200

Ala Lys Glu Thr Ala Leu Asn Asp Ile Asn Gln Ala Gln Thr Asn  
1205 1210 1215

Gln Asn Val Asp Thr Ala Leu Thr Ser Gly Ile Gln Asn Ile Gln  
1220 1225 1230

Asn Thr Gln Val Asn Val Arg Lys Lys Gln Glu Ala Lys Thr Thr  
1235 1240 1245

Ile Asn Asp Ile Val Gln Gln His Lys Gln Thr Ile Gln Asn Asn  
1250 1255 1260

Asp Asp Ala Thr Thr Glu Glu Lys Glu Val Ala Asn Asn Leu Val  
1265 1270 1275

Asn Ala Ser Gln Gln Asn Val Ile Ser Lys Ile Asp Asn Ala Thr  
1280 1285 1290

Thr Asn Asn Gln Ile Asp Gly Ile Val Ser Asp Gly Arg Gln Ser  
1295 1300 1305

Ile Asn Ala Ile Thr Pro Asp Thr Ser Ile Lys Arg Asn Ala Lys  
1310 1315 1320

Asn Asp Ile Asp Ile Lys Ala Ala Asp Lys Lys Ile Lys Ile Gln  
1325 1330 1335

Arg Ile Asn Asp Ala Thr Asp Glu Glu Ile Gln Glu Ala Asn Arg  
1340 1345 1350

Lys Ile Glu Glu Ala Lys Ile Glu Ala Lys Asp Asn Ile Gln Arg  
1355 1360 1365

Asn Ser Thr Arg Asp Gln Val Asn Glu Ala Lys Thr Asn Gly Ile  
1370 1375 1380

Asn Lys Ile Glu Asn Ile Thr Pro Ala Thr Thr Val Lys Ser Glu  
1385 1390 1395

Ala Arg Gln Ala Val Gln Asn Lys Ala Asn Glu Gln Ile Asn His  
1400 1405 1410

Ile Gln Asn Thr Pro Asp Ala Thr Asn Glu Glu Lys Gln Glu Ala  
1415 1420 1425

Ile Asn Arg Val Ser Ala Glu Leu Ala Arg Val Gln Ala Gln Ile  
1430 1435 1440

Asn Ala Glu His Thr Thr Gln Gly Val Lys Thr Ile Lys Asp Asp  
1445 1450 1455

Ala Ile Thr Ser Leu Ser Arg Ile Asn Ala Gln Val Val Glu Lys  
1460 1465 1470

Glu Ser Ala Arg Asn Ala Ile Glu Gln Lys Ala Thr Gln Gln Thr  
1475 1480 1485

Gln Phe Ile Asn Asn Asn Asp Asn Ala Thr Asp Glu Glu Lys Glu  
1490 1495 1500

Val Ala Asn Asn Leu Val Ile Ala Thr Lys Gln Lys Ser Leu Asp  
1505 1510 1515

Asn Ile Asn Ser Leu Ser Ser Asn Asn Asp Val Glu Asn Ala Lys  
1520 1525 1530

Val Ala Gly Ile Asn Glu Ile Ala Asn Val Leu Pro Ala Thr Ala  
1535 1540 1545

Val Lys Ser Lys Ala Lys Lys Asp Ile Asp Gln Lys Leu Ala Gln  
1550 1555 1560

Gln Ile Asn Gln Ile Gln Thr His Gln Thr Ala Thr Thr Glu Glu  
1565 1570 1575

Lys Glu Ala Ala Ile Gln Leu Ala Asn Gln Lys Ser Asn Glu Ala  
1580 1585 1590

Arg Thr Ala Ile Gln Asn Glu His Ser Asn Asn Gly Val Ala Gln  
1595 1600 1605

Ala Lys Ser Asn Gly Ile His Glu Ile Glu Leu Val Met Pro Asp  
1610 1615 1620

Ala His Lys Lys Ser Asp Ala Lys Gln Ser Ile Asp Asn Lys Tyr  
1625 1630 1635

Asn Glu Gln Ser Asn Thr Ile Asn Thr Thr Pro Asp Ala Thr Asp  
1640 1645 1650

Glu Glu Lys Gln Lys Ala Leu Asp Lys Leu Lys Ile Ala Lys Asp  
1655 1660 1665

Ala Gly Tyr Asn Lys Val Asp Gln Ala Gln Thr Asn Gln Gln Val  
1670 1675 1680

Ser Asp Ala Lys Thr Glu Ala Ile Asp Thr Ile Thr Asn Ile Gln  
1685 1690 1695

Ala Asn Val Ala Lys Lys Pro Ser Ala Arg Val Glu Leu Asp Ser  
1700 1705 1710

Lys Phe Glu Asp Leu Lys Arg Gln Ile Asn Ala Thr Pro Asn Ala  
1715 1720 1725

Thr Glu Glu Glu Lys Gln Asp Ala Ile Gln Arg Leu Asn Gly Lys  
1730 1735 1740

Arg Asp Glu Val Lys Asn Leu Ile Asn Gln Asp Arg Arg Asp Asn  
1745 1750 1755

Glu Val Glu Gln His Lys Asn Ile Gly Leu Gln Glu Leu Glu Thr  
1760 1765 1770

Ile His Ala Asn Pro Thr Arg Lys Ser Asp Ala Leu Gln Glu Leu  
1775 1780 1785

Gln Thr Lys Phe Ile Ser Gln Thr Glu Leu Ile Asn Asn Asn Lys  
1790 1795 1800

Asp Ala Thr Asn Glu Glu Lys Asp Glu Ala Lys Arg Leu Leu Glu  
1805 1810 1815

Ile Ser Lys Asn Lys Thr Ile Thr Asn Ile Asn Gln Ala Gln Thr  
1820 1825 1830

Asn Asn Gln Val Asp Asn Ala Lys Asp Asn Gly Met Asn Glu Ile  
1835 1840 1845

Ala Thr Ile Ile Pro Ala Thr Thr Ile Lys Thr Asp Ala Lys Thr  
1850 1855 1860

Ala Ile Asp Lys Lys Ala Glu Gln Gln Val Thr Ile Ile Asn Gly  
1865 1870 1875

Asn Asn Asp Ala Thr Asp Glu Glu Lys Ala Glu Ala Arg Lys Leu  
1880 1885 1890

Val Glu Lys Ala Lys Ile Glu Ala Lys Ser Asn Ile Thr Asn Ser  
1895 1900 1905

Asp Thr Glu Arg Glu Val Asn Gly Ala Lys Thr Asn Gly Leu Glu  
1910 1915 1920

Lys Ile Asn Asn Ile Gln Pro Ser Thr Gln Thr Lys Thr Asn Ala  
1925 1930 1935

Lys Gln Glu Ile Asn Asp Lys Ala Gln Glu Gln Leu Ile Gln Ile

1940

1945

1950

Asn Asn Thr Pro Asp Ala Thr Glu Glu Glu Lys Gln Glu Ala Thr  
1955 1960 1965

Asn Arg Val Asn Ala Gly Leu Ala Gln Ala Ile Gln Asn Ile Asn  
1970 1975 1980

Asn Ala His Ser Thr Gln Glu Val Asn Glu Ser Lys Thr Asn Ser  
1985 1990 1995

Ile Ala Thr Ile Lys Ser Val Gln Pro Asn Val Ile Lys Lys Pro  
2000 2005 2010

Thr Ala Ile Asn Ser Leu Thr Gln Glu Ala Asn Asn Gln Lys Thr  
2015 2020 2025

Leu Ile Gly Asn Asp Gly Asn Ala Thr Asp Asp Glu Lys Glu Ala  
2030 2035 2040

Ala Lys Gln Leu Val Thr Gln Lys Leu Asn Glu Gln Ile Gln Lys  
2045 2050 2055

Ile His Glu Ser Thr Gln Asp Asn Gln Val Asp Asn Val Lys Ala  
2060 2065 2070

Gln Ala Ile Thr Ala Ile Lys Leu Ile Asn Ala Asn Ala His Lys  
2075 2080 2085

Arg Gln Asp Ala Ile Asn Ile Leu Thr Asn Leu Ala Glu Ser Lys  
2090 2095 2100

Lys Ser Asp Ile Arg Ala Asn Gln Asp Ala Thr Thr Glu Glu Lys  
2105 2110 2115

Asn Thr Ala Ile Gln Ser Ile Asp Asp Thr Leu Ala Gln Ala Arg  
2120 2125 2130

Asn Asn Ile Asn Gly Ala Asn Thr Asn Ala Leu Val Asp Glu Asn  
2135 2140 2145

Leu Glu Asp Gly Lys Gln Lys Leu Gln Arg Ile Val Leu Ser Thr  
2150 2155 2160

Gln Thr Lys Thr Gln Ala Lys Ala Asp Ile Ala Gln Ala Ile Gly  
2165 2170 2175

Gln Gln Arg Ser Thr Ile Asp Gln Asn Gln Asn Ala Thr Thr Glu  
2180 2185 2190

Glu Lys Gln Glu Ala Leu Glu Arg Leu Asn Gln Glu Thr Asn Gly  
2195 2200 2205

Val Asn Asp Arg Ile Gln Ala Ala Leu Ala Asn Gln Asn Val Thr  
2210 2215 2220

Asp Glu Lys Asn Asn Ile Leu Glu Thr Ile Arg Asn Val Glu Pro  
2225 2230 2235

Ile Val Ile Val Lys Pro Lys Ala Asn Glu Ile Ile Arg Lys Lys  
2240 2245 2250

Ala Ala Glu Gln Thr Thr Leu Ile Asn Gln Asn Gln Asp Ala Thr  
2255 2260 2265

Leu Glu Glu Lys Gln Ile Ala Leu Gly Lys Leu Glu Glu Val Lys  
2270 2275 2280

Asn Glu Ala Leu Asn Gln Val Ser Gln Ala His Ser Asn Asn Asp  
2285 2290 2295

Val Lys Ile Val Glu Asn Asn Gly Ile Ala Lys Ile Ser Glu Val  
2300 2305 2310

His Pro Glu Thr Ile Ile Lys Arg Asn Ala Lys Gln Glu Ile Glu  
2315 2320 2325

Gln Asp Ala Gln Ser Gln Ile Asp Thr Ile Asn Ala Asn Asn Lys  
2330 2335 2340

Ser Thr Asn Glu Glu Lys Ser Ala Ala Ile Asp Arg Val Asn Val  
2345 2350 2355

Ala Lys Ile Asp Ala Ile Asn Asn Ile Thr Asn Ala Thr Thr Thr  
2360 2365 2370

Gln Leu Val Asn Asp Ala Lys Asn Ser Gly Asn Thr Ser Ile Ser  
2375 2380 2385

Gln Ile Leu Pro Ser Thr Ala Val Lys Thr Asn Ala Leu Ala Ala  
2390 2395 2400

Leu Ala Ser Glu Ala Lys Asn Lys Asn Ala Ile Ile Asp Gln Thr  
2405 2410 2415

Pro Asn Ala Thr Ala Glu Glu Lys Glu Glu Ala Asn Asn Lys Val  
2420 2425 2430

Asp Arg Leu Gln Glu Glu Ala Asp Ala Asn Ile Leu Lys Ala His  
2435 2440 2445

Thr Thr Asp Glu Val Asn Asn Ile Lys Asn Gln Ala Val Gln Asn  
2450 2455 2460

Ile Asn Ala Val Gln Val Glu Val Ile Lys Lys Gln Asn Ala Lys  
2465 2470 2475

Asn Gln Leu Asn Gln Phe Ile Asp Asn Gln Lys Lys Ile Ile Glu  
2480 2485 2490

Asn Thr Pro Asp Ala Thr Leu Glu Glu Lys Ala Glu Ala Asn Arg  
2495 2500 2505

Leu Leu Gln Asn Val Leu Thr Ser Thr Ser Asp Glu Ile Ala Asn  
2510 2515 2520

Val Asp His Asn Asn Glu Val Asp Gln Ala Leu Asp Lys Ala Arg  
2525 2530 2535

Pro Lys Ile Glu Ala Ile Val Pro Gln Val Ser Lys Lys Arg Asp  
2540 2545 2550

Ala Leu Asn Ala Ile Gln Glu Ala Phe Asn Ser Gln Thr Gln Glu  
2555 2560 2565

Ile Gln Glu Asn Gln Glu Ala Thr Asn Glu Glu Lys Thr Glu Ala  
2570 2575 2580

Leu Asn Lys Ile Asn Gln Leu Leu Asn Gln Ala Lys Val Asn Ile  
2585 2590 2595

Asp Gln Ala Gln Ser Asn Lys Asp Val Asp Ser Ala Lys Thr Arg  
2600 2605 2610

Ser Ile Gln Asp Ile Glu Gln Ile Gln Pro His Pro Gln Thr Lys  
2615 2620 2625

Ala Thr Gly Arg His Arg Leu Asn Glu Lys Ala Asn Gln Gln Gln  
2630 2635 2640

Ser Thr Ile Ala Thr His Pro Asn Ser Thr Ile Glu Glu Arg Gln  
2645 2650 2655

Glu Ala Ser Ala Lys Leu Gln Glu Val Leu Lys Lys Ala Ile Ala  
2660 2665 2670

Lys Ile Asp Lys Gly Gln Thr Asn Asp Asp Val Glu Lys Thr Val  
2675 2680 2685

Val Asn Gly Ile Ala Glu Ile Glu Asn Ile Leu Pro Ala Thr Thr  
2690 2695 2700

Val Lys Asp Lys Ala Lys Ala Asp Val Asn Ala Glu Lys Glu Glu  
2705 2710 2715

Lys Asn Leu Gln Ile Asn Ser Asn Asp Glu Ala Thr Thr Glu Glu  
2720 2725 2730

Lys Leu Val Ala Ser Asp Asn Leu Asn His Val Val Glu Thr Thr  
2735 2740 2745

Asn Gln Ala Ile Glu Asp Ala Pro Asp Thr Asn Gln Val Asn Val  
2750 2755 2760

Glu Lys Asn Lys Gly Ile Gly Thr Ile Arg Asp Ile Gln Pro Leu  
2765 2770 2775

Val Val Lys Lys Pro Thr Ala Lys Ser Lys Ile Glu Ser Ala Val  
2780 2785 2790

Glu Lys Lys Lys Thr Glu Ile Asn Gln Thr Gln Asn Ala Thr His  
2795 2800 2805

Asp Glu Val Arg Glu Gly Leu Asn Gln Leu Asn Gln Ile His Glu  
2810 2815 2820

Lys Ala Lys Asn Asp Val Asn Gln Ser Gln Thr Asn Gln Gln Val  
2825 2830 2835

Glu Asn Ala Glu Gln Asn Ser Leu Asp Gln Ile Asn Asn Phe Arg  
2840 2845 2850

Pro Asp Phe Ser Lys Lys Arg Asn Ala Val Ala Glu Ile Val Lys

2855

2860

2865

Ala Gln Gln Asn Lys Ile Asp Glu Ile Glu Gln Glu Phe Ser Ala  
2870 2875 2880

Thr Gln Glu Glu Lys Asp Asn Ala Leu Gln His Leu Asp Glu Gln  
2885 2890 2895

Val Lys Glu Ile Ile Asn Ser Ile Asn Gln Ala Asn Thr Asp Asn  
2900 2905 2910

Glu Val Asp Asn Ala Lys Thr Ser Gly Leu Asn Asn Ile Thr Glu  
2915 2920 2925

Tyr Arg Pro Glu Tyr Asn Lys Lys Lys Asn Ala Ile Leu Lys Leu  
2930 2935 2940

Tyr Asp Val Ser Asp Thr Gln Glu Ala Ile Ile Asn Gly Tyr Pro  
2945 2950 2955

Asp Ala Thr Glu Asp Glu Leu Gln Glu Ala Asn Ser Lys Leu Asn  
2960 2965 2970

Lys Ile Leu Leu Asp Ala Lys Lys Gln Ile Gly Leu Ala His Thr  
2975 2980 2985

Asn Asn Glu Val Asp Asp Ile Tyr Asn Glu Val Ser Gln Lys Met  
2990 2995 3000

Lys Thr Ile Leu Pro Arg Val Asp Thr Lys Ala Val Ala Arg Ser  
3005 3010 3015

Val Leu Asn Ala Leu Ala Lys Gln Leu Ile Lys Thr Phe Glu Asn  
3020 3025 3030

Thr Ala Asp Val Thr His Glu Glu Arg Asn Asp Ala Ile Asn His  
3035 3040 3045

Val Lys Glu Gln Leu Ser Leu Val Phe Asn Ala Ile Glu Lys Asp  
3050 3055 3060

Arg Lys Asp Ile Gln Val Ala Gln Asp Glu Leu Phe Gly Leu Asn  
3065 3070 3075

Glu Leu Asn Ser Ile Phe Ile Asn Ile Thr Gln Lys Pro Thr Ala  
3080 3085 3090

Arg Lys Ala Ile Ser Gly Met Ala Ser Gln Leu Asn Asn Ser Ile  
3095 3100 3105

Asn Asn Thr Pro Tyr Ala Thr Glu Glu Glu Arg Gln Ile Ala Leu  
3110 3115 3120

Asn Lys Val Lys Ala Ile Val Asp Asp Ala Asn Glu Lys Ile Arg  
3125 3130 3135

Glu Ala Asn Thr Asp Ser Glu Val Leu Gly Thr Lys Ser Asn Ala  
3140 3145 3150

Ile Thr Leu Leu Gln Ala Ile Ser Ala Asp Val Gln Val Lys Pro  
3155 3160 3165

Gln Ala Phe Glu Glu Ile Asn Ala Gln Ala Glu Ile Gln Arg Glu  
3170 3175 3180

Arg Ile Asn Gly Asn Ser Asp Ala Thr Arg Glu Glu Lys Glu Glu  
3185 3190 3195

Ala Leu Lys Gln Val Asp Thr Leu Val Asn His Ser Phe Ile Thr  
3200 3205 3210

Ile Asn Asn Val Asn Lys Asn Gln Glu Val Tyr Asp Thr Lys Asp  
3215 3220 3225

Lys Thr Ile Glu Ala Ile His Lys Ile Lys Pro Ile Ser Thr Ile  
3230 3235 3240

Lys Pro Gln Ala Leu Asn Glu Ile Thr Ile Gln Leu Asp Thr Gln  
3245 3250 3255

Arg Asp Leu Ile Lys Asn Asn Lys Glu Ser Thr Val Glu Glu Lys  
3260 3265 3270

Ala Ser Ala Ile Asp Lys Leu Ile Lys Thr Ala Ala Arg Ile Ala  
3275 3280 3285

Glu Ser Ile Asp Lys Ala Gln Thr Asn Glu Glu Val Lys Asn Ile  
3290 3295 3300

Lys Lys Gln Ser Ile Asp Glu Ile Ser Lys Ile Leu Pro Val Ile  
3305 3310 3315

Glu Ile Lys Ser Ala Ala Arg Asn Glu Ile His Gln Lys Ala Glu  
3320 3325 3330

Val Ile Arg Gly Leu Ile Asn Asp Asn Glu Glu Ala Thr Lys Glu  
3335 3340 3345

Glu Lys Asp Ile Ala Leu Asn Gln Leu Asp Thr Thr Leu Thr Gln  
3350 3355 3360

Ala Asn Val Ser Ile Asp Gln Ala Leu Thr Asn Glu Ala Val Asn  
3365 3370 3375

Arg Ala Lys Glu Ile Ala Asn Ser Glu Ile Asn Lys Ile Ser Val  
3380 3385 3390

Ile Ala Ile Lys Lys Pro Glu Ala Ile Ala Glu Ile Gln Glu Leu  
3395 3400 3405

Ala Asp Lys Lys Leu Asn Lys Phe Lys Gln Ser Gln Glu Ala Thr  
3410 3415 3420

Ile Glu Glu Lys Gln Ser Ala Ile Asn Glu Leu Glu Gln Ala Leu  
3425 3430 3435

Lys Ser Ala Ile Asn His Ile His Gln Ser Gln Asn Asn Glu Ser  
3440 3445 3450

Val Ser Ala Ala Leu Lys Glu Ser Ile Ser Leu Ile Asp Ser Ile  
3455 3460 3465

Glu Ile Gln Ala His Lys Lys Leu Glu Ala Lys Ala Tyr Ile Asp  
3470 3475 3480

Gly Tyr Ser Asp Asp Lys Ile Asn Asp Ile Ser Ser Arg Ala Thr  
3485 3490 3495

Asn Glu Glu Lys Gln Ile Phe Val Ser Lys Leu Lys Ala Leu Ile  
3500 3505 3510

Asn Arg Thr His Lys Gln Ile Asp Glu Ala Glu Thr Phe Val Ser  
3515 3520 3525

Val Glu Thr Ile Val Arg Asn Phe Lys Val Glu Ala Asp Lys Leu  
3530 3535 3540

Asn	Ser	Ile	Val	Arg	Lys	Lys	Ala	Lys	Ala	Ser	Lys	Glu	Ile	Glu
3545														
3550														
3555														
Leu	Glu	Ala	Asp	His	Val	Lys	Gln	Met	Ile	Asn	Ala	Asn	Leu	Ser
3560														
3565														
3570														
Ala	Ser	Thr	Arg	Val	Lys	Gln	Asn	Ala	Arg	Thr	Leu	Ile	Asn	Glu
3575														
3580														
3585														
Ile	Val	Ser	Asn	Ala	Leu	Ser	Gln	Leu	Asn	Lys	Val	Thr	Thr	Asn
3590														
3595														
3600														
Lys	Glu	Val	Asp	Glu	Ile	Val	Asn	Glu	Thr	Ile	Glu	Lys	Leu	Lys
3605														
3610														
3615														
Ser	Ile	Gln	Ile	Arg	Glu	Asp	Lys	Ile	Leu	Ser	Ser	Gln	Arg	Ser
3620														
3625														
3630														
Ser	Thr	Ser	Met	Thr	Glu	Lys	Ser	Asn	Gln	Cys	Tyr	Ser	Ser	Glu
3635														
3640														
3645														
Asn	Asn	Thr	Ile	Lys	Ser	Leu	Pro	Glu	Ala	Gly	Asn	Ala	Asp	Lys
3650														
3655														
3660														
Ser	Leu	Pro	Leu	Ala	Gly	Val	Thr	Leu	Ile	Ser	Gly	Leu	Ala	Ile
3665														
3670														
3675														
Met	Ser	Ser	Arg	Lys	Lys	Lys	Asp	Lys	Lys	Val	Asn	Asp		
3680														
3685														
3690														
<210> 49														
<211> 439														
<212> PRT														
<213> Staphylococcus epidermidis														
<400> 49														
Leu	Asp	Ile	Lys	Met	Pro	Lys	Leu	Gly	Glu	Ser	Val	His	Glu	Gly
1														
5														
10														
15														
Ile	Glu	Gln	Trp	Leu	Val	Ser	Val	Gly	Asp	His	Val	Asp	Glu	Tyr
20														
25														
30														
Pro	Leu	Cys	Glu	Val	Ile	Thr	Asp	Lys	Val	Thr	Ala	Glu	Val	Pro
35														
40														
45														
Thr	Ile	Ser	Gly	Thr	Ile	Thr	Glu	Leu	Val	Val	Glu	Glu	Gly	Gln
50														
55														
60														

Val Asn Ile Asn Thr Val Ile Cys Lys Ile Asp Ser Glu Asn Gly Gln  
65 70 75 80

Asn Gln Thr Glu Ser Ala Asn Glu Phe Lys Glu Glu Gln Asn Gln His  
85 90 95

Ser Gln Ser Asn Ile Asn Val Ser Gln Phe Glu Asn Asn Pro Lys Thr  
100 105 110

His Glu Ser Glu Val His Thr Ala Ser Ser Arg Ala Asn Asn Asn Gly  
115 120 125

Arg Phe Ser Pro Val Val Phe Lys Leu Ala Ser Glu His Asp Ile Asp  
130 135 140

Leu Thr Gln Val Lys Gly Thr Gly Phe Glu Gly Arg Val Thr Lys Lys  
145 150 155 160

Asp Ile Gln Asn Ile Ile Asn Asn Pro Asn Asp Gln Glu Lys Glu Lys  
165 170 175

Glu Phe Lys Gln Thr Asp Lys Lys Asp His Ser Thr Asn His Cys Asp  
180 185 190

Phe Leu His Gln Ser Ser Thr Lys Asn Glu His Ser Pro Leu Ser Asn  
195 200 205

Glu Arg Val Val Pro Val Lys Gly Ile Arg Lys Ala Ile Ala Gln Asn  
210 215 220

Met Val Thr Ser Val Ser Glu Ile Pro His Gly Trp Met Met Val Glu  
225 230 235 240

Ala Asp Ala Thr Asn Leu Val Gln Thr Arg Asn Tyr His Lys Ala Gln  
245 250 255

Phe Lys Gln Asn Glu Gly Tyr Asn Leu Thr Phe Phe Ala Phe Phe Val  
260 265 270

Lys Ala Val Ala Glu Ala Leu Lys Val Asn Pro Leu Leu Asn Ser Thr  
275 280 285

Trp Gln Gly Asp Glu Ile Val Ile His Lys Asp Ile Asn Ile Ser Ile  
290 295 300

Ala Val Ala Asp Asp Asp Lys Leu Tyr Val Pro Val Ile Lys Asn Ala  
305 310 315 320

Asp Glu Lys Ser Ile Lys Gly Ile Ala Arg Glu Ile Asn Asp Leu Ala  
325 330 335

Thr Lys Ala Arg Leu Gly Lys Leu Ala Gln Ser Asp Met Gln Asn Gly  
340 345 350

Thr Phe Thr Val Asn Asn Thr Gly Ser Phe Gly Ser Val Ser Ser Met  
355 360 365

Gly Ile Ile Asn His Pro Gln Ala Ala Ile Leu Gln Val Glu Ser Val  
370 375 380

Val Lys Lys Pro Val Val Ile Asp Asp Met Ile Ala Ile Arg Asn Met  
385 390 395 400

Val Asn Leu Cys Ile Ser Ile Asp His Arg Ile Leu Asp Gly Val Gln  
405 410 415

Thr Gly Lys Phe Met Asn Leu Val Lys Lys Lys Ile Glu Gln Tyr Ser  
420 425 430

Ile Glu Asn Thr Ser Ile Tyr  
435

<210> 50  
<211> 295  
<212> PRT  
<213> *Staphylococcus epidermidis*  
  
<400> 50

Met Asn Thr Ile Ile Glu Glu Tyr Leu Asn Phe Ile Gln Ile Glu Lys  
1 5 10 15

Gly Leu Ser Asn Asn Thr Ile Gly Ala Tyr Arg Arg Asp Leu Lys Lys  
20 25 30

Tyr Lys Asp Tyr Leu Glu Asp Asn Lys Ile Ser His Ile Asp Phe Ile  
35 40 45

Asp Arg Gln Ile Ile Gln Glu Cys Leu Gly His Leu Ile Asp Met Gly  
50 55 60

Gln Ser Ser Lys Ser Leu Ala Arg Phe Ile Ser Thr Ile Arg Ser Phe

65

70

75

80

His Gln Phe Ala Leu Arg Glu Lys Tyr Ala Ala Lys Asp Pro Thr Val  
 85 90 95

Leu Ile Glu Thr Pro Lys Tyr Glu Lys Lys Leu Pro Asp Val Leu Glu  
 100 105 110

Ile Asp Glu Val Ile Ala Leu Leu Glu Thr Pro Asp Leu Thr Lys Asn  
 115 120 125

Asn Gly Tyr Arg Asp Arg Thr Met Leu Glu Leu Leu Tyr Ala Thr Gly  
 130 135 140

Met Arg Val Thr Glu Ile Ile Gln Leu Asp Val Glu Asp Val Asn Leu  
 145 150 155 160

Met Met Gly Phe Val Arg Val Phe Gly Lys Gly Asn Lys Glu Arg Ile  
 165 170 175

Val Pro Leu Gly Asp Thr Val Ile Glu Tyr Leu Thr Thr Tyr Ile Glu  
 180 185 190

Thr Val Arg Pro Gln Leu Leu Lys Gln Thr Thr Gln Ala Leu Phe  
 195 200 205

Leu Asn Met His Gly Lys Ser Leu Ser Arg Gln Gly Ile Trp Lys Ile  
 210 215 220

Ile Lys Gln Tyr Gly Leu Lys Ala Asn Ile Asn Lys Thr Leu Thr Pro  
 225 230 235 240

His Thr Leu Arg His Ser Phe Ala Thr His Leu Leu Glu Asn Gly Ala  
 245 250 255

Asp Leu Arg Ala Val Gln Glu Met Leu Gly His Ser Asp Ile Ser Thr  
 260 265 270

Thr Gln Leu Tyr Thr His Val Ser Lys Ser Gln Ile Arg Lys Met Tyr  
 275 280 285

Thr Gln Phe His Pro Arg Ala  
 290 295

<210> 51  
 <211> 800

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 51

Met Ser Leu Val Tyr Leu Met Ala Thr Asn Leu Leu Val Met Leu Ile  
1 5 10 15

Val Leu Phe Thr Leu Ser His Arg Gln Leu Arg Lys Val Ala Gly Tyr  
20 25 30

Val Ala Leu Ile Ala Pro Ile Val Thr Ser Thr Tyr Phe Ile Met Lys  
35 40 45

Ile Pro Asp Val Ile Arg Asn Lys Phe Ile Ala Val Arg Leu Pro Trp  
50 55 60

Met Pro Ser Ile Asp Ile Asn Leu Asp Leu Arg Leu Asp Gly Leu Ser  
65 70 75 80

Leu Met Phe Gly Leu Ile Ile Ser Leu Ile Gly Val Gly Val Phe Phe  
85 90 95

Tyr Ala Thr Gln Tyr Leu Ser His Ser Thr Asp Asn Leu Pro Arg Phe  
100 105 110

Phe Ile Tyr Leu Leu Phe Met Phe Ser Met Ile Gly Ile Val Ile  
115 120 125

Ala Asn Asn Thr Ile Leu Met Tyr Val Phe Trp Glu Leu Thr Ser Ile  
130 135 140

Ser Ser Phe Leu Leu Ile Ser Tyr Trp Tyr Asn Asn Gly Glu Ser Gln  
145 150 155 160

Leu Gly Ala Ile Gln Ser Phe Met Ile Thr Val Phe Gly Gly Leu Ala  
165 170 175

Leu Leu Thr Gly Phe Ile Ile Leu Tyr Ile Ile Thr Gly Thr Asn Thr  
180 185 190

Ile Thr Asp Ile Leu Asn Gln Arg Asn Ala Ile Ser Arg His Pro Leu  
195 200 205

Phe Ile Pro Met Ile Leu Met Leu Leu Leu Gly Ala Phe Thr Lys Ser  
210 215 220

Ala Gln Phe Pro Phe His Ile Trp Leu Pro Lys Ala Met Ala Ala Pro  
225 230 235 240

Thr Pro Val Ser Ala Tyr Leu His Ser Ala Thr Met Val Lys Ala Gly  
245 250 255

Ile Phe Leu Leu Phe Arg Phe Thr Pro Leu Leu Gly Leu Ser Asn Val  
260 265 270

Tyr Ile Tyr Thr Val Thr Phe Val Gly Leu Ile Thr Met Leu Phe Gly  
275 280 285

Ser Leu Thr Ala Leu Arg Gln Tyr Asp Leu Lys Gly Ile Leu Ala Tyr  
290 295 300

Ser Thr Ile Ser Gln Leu Gly Met Ile Met Thr Met Val Gly Leu Gly  
305 310 315 320

Gly Gly Tyr Ala Gln His Thr Ser Asp Glu Leu Ser Lys Phe Tyr Ile  
325 330 335

Leu Val Leu Phe Ala Gly Leu Phe His Leu Met Asn His Ala Val Phe  
340 345 350

Lys Cys Ala Leu Phe Met Gly Val Gly Ile Ile Asp His Glu Ser Gly  
355 360 365

Thr Arg Asp Ile Arg Leu Leu Asn Gly Met Arg Lys Val Phe Pro Lys  
370 375 380

Met His Ile Val Met Leu Leu Ala Ala Leu Ser Met Ala Gly Val Pro  
385 390 395 400

Phe Leu Asn Gly Phe Leu Ser Lys Glu Met Phe Leu Asp Ser Leu Thr  
405 410 415

Lys Ala Asn Glu Leu Asp Gln Tyr Gly Phe Val Leu Thr Phe Val Ile  
420 425 430

Ile Ser Ile Gly Val Ile Ala Ser Ile Leu Thr Phe Thr Tyr Ala Leu  
435 440 445

Tyr Met Ile Lys Glu Thr Phe Trp Gly Asn Tyr Asn Ile Glu Lys Phe  
450 455 460

Lys Arg Lys Gln Ile His Glu Pro Trp Leu Phe Ser Leu Pro Ala Val

465

470

475

480

Ile Leu Met Leu Leu Ile Pro Val Ile Phe Phe Val Pro Asn Val Phe  
485 490 495

Gly Asn Phe Val Ile Leu Pro Ala Thr Arg Ser Val Ser Gly Ile Gly  
500 505 510

Ala Glu Val Asp Ala Phe Val Pro His Ile Ser Gln Trp His Gly Val  
515 520 525

Asn Leu Pro Leu Ile Leu Ser Ile Val Val Ile Ile Ile Gly Leu Ile  
530 535 540

Leu Ala Leu Val Val Asn Trp Lys Glu Val Thr His Gln Ile Ile Lys  
545 550 555 560

Ser Ala Ser Ile Thr Asp Gly Tyr Arg Lys Ile Tyr Arg Glu Phe Glu  
565 570 575

Leu Tyr Ser Ala Arg Gly Ile Arg Ala Leu Met Asn Asn Lys Leu Asn  
580 585 590

Tyr Tyr Ile Met Ile Thr Leu Phe Ile Phe Val Ala Ile Val Val Tyr  
595 600 605

Gly Tyr Leu Thr Val Gly Phe Pro His Val His Gln Leu His Ile Ser  
610 615 620

Ser Phe Gly Pro Leu Glu Val Ile Leu Ser Val Val Thr Leu Ile Ile  
625 630 635 640

Gly Ile Ser Leu Ile Phe Ile Arg Gln Arg Leu Thr Met Val Val Leu  
645 650 655

Asn Gly Met Ile Gly Phe Ala Val Thr Leu Tyr Phe Ile Ala Met Lys  
660 665 670

Ala Pro Asp Leu Ala Leu Thr Gln Leu Val Val Glu Thr Ile Thr Thr  
675 680 685

Ile Leu Phe Ile Val Ser Phe Ser Arg Leu Pro Asn Ile Pro Arg Val  
690 695 700

Lys Ala Asn Leu Lys Lys Glu Thr Phe Lys Ile Ile Val Ser Leu Val  
705 710 715 720

Met Ala Leu Thr Val Val Ser Leu Ile Phe Val Ala Gln Gln Ala Asp  
725 730 735

Gly Met Pro Ser Ile Ala Lys Phe Tyr Glu Asp Ala Tyr Glu Leu Thr  
740 745 750

Gly Gly Lys Asn Ile Val Asn Ala Ile Leu Gly Asp Phe Arg Ala Leu  
755 760 765

Asp Thr Met Phe Glu Gly Leu Val Leu Ile Ile Ala Gly Leu Gly Ile  
770 775 780

Tyr Thr Leu Leu Asn Tyr Lys Asp Arg Arg Gly Gln Asp Glu Arg Glu  
785 790 795 800

<210> 52  
<211> 892  
<212> PRT  
<213> Staphylococcus epidermidis

<400> 52

Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Thr Val  
1 5 10 15

Gln Asp Val Lys Asp Ser Asn Met Asp Asp Glu Leu Ser Asp Ser Asn  
20 25 30

Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp Val Ile Asn Asn Ser Gln  
35 40 45

Ser Ile Asn Thr Asp Asp Asp Asn Gln Ile Lys Lys Glu Glu Thr Asn  
50 55 60

Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys Asp Ile Thr Gln Ser Thr  
65 70 75 80

Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln  
85 90 95

Asp Asn Thr Gln Leu Lys Glu Glu Val Val Lys Glu Pro Ser Ser Val  
100 105 110

Glu Ser Ser Asn Ser Ser Met Asp Thr Ala Gln Gln Pro Ser His Thr  
115 120 125

Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr Ser Asp Asn Glu Glu Asn  
130 135 140

Ser Arg Val Ser Asp Phe Ala Asn Ser Lys Ile Ile Glu Ser Asn Thr  
145 150 155 160

Glu Ser Asn Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Arg  
165 170 175

Glu Asp Ser Ile Thr Ser Gln Pro Ser Ser Tyr Lys Asn Ile Asp Glu  
180 185 190

Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr  
195 200 205

Glu Asn Lys Val Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ser  
210 215 220

Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val  
225 230 235 240

Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp  
245 250 255

Asp Ser Asp Gly Ile Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr  
260 265 270

Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met  
275 280 285

Thr Val Asn Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser  
290 295 300

Phe Ala Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr  
305 310 315 320

Gly Thr Tyr Asp Asn Thr Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp  
325 330 335

Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser  
340 345 350

Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val  
355 360 365

Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu

370

375

380

Tyr Gln Lys Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe  
 385 390 395 400

Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile  
 405 410 415

Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly  
 420 425 430

Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys  
 435 440 445

Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile  
 450 455 460

Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln  
 465 470 475 480

Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser  
 485 490 495

Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp  
 500 505 510

Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu  
 515 520 525

Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe  
 530 535 540

Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr  
 545 550 555 560

Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile  
 565 570 575

Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr  
 580 585 590

Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Glu  
 595 600 605

Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr Lys Ile  
 610 615 620

Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His Ser Gly  
625 630 635 640

Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val Thr Ile  
645 650 655

Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln Thr Pro  
660 665 670

Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys Asp Gly  
675 680 685

Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu  
690 695 700

Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Asp Glu Asn  
705 710 715 720

Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile Val His  
725 730 735

Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Asp Ser Gly Asp  
740 745 750

Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr Ile Thr  
755 760 765

Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp Asp Ser  
770 775 780

Asp Ser Asp  
785 790 795 800

Ser Asp  
805 810 815

Ser Asp  
820 825 830

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn  
835 840 845

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser  
850 855 860

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu  
865 870 875 880

Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn  
885 890

<210> 53  
<211> 484  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 53

Met Ser Glu Arg Ile Arg Val Arg Tyr Ala Pro Ser Pro Thr Gly Tyr  
1 5 10 15

Leu His Ile Gly Asn Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala  
20 25 30

Lys His Tyr Asn Gly Asp Phe Val Val Arg Ile Glu Asp Thr Asp Ser  
35 40 45

Lys Arg Asn Leu Glu Asp Gly Glu Ser Ser Gln Phe Asp Asn Leu Lys  
50 55 60

Trp Leu Gly Leu Asp Trp Asp Glu Ser Val Asp Lys Asp Lys Gly Phe  
65 70 75 80

Gly Pro Tyr Arg Gln Ser Glu Arg Ala Glu Ile Tyr Asn Pro Leu Ile  
85 90 95

Gln Gln Leu Leu Glu Glu Asp Lys Ala Tyr Lys Cys Tyr Met Thr Glu  
100 105 110

Glu Glu Leu Glu Ala Glu Arg Glu Ala Gln Ile Ala Arg Gly Glu Met  
115 120 125

Pro Arg Tyr Gly Gly Gln His Ala His Leu Thr Glu Glu Gln Arg Gln  
130 135 140

Gln Tyr Glu Ala Glu Gly Arg Lys Pro Ser Ile Arg Phe Arg Val Pro  
145 150 155 160

Lys Asp Gln Thr Tyr Thr Phe Asn Asp Met Val Lys Gly Glu Ile Ser  
165 170 175

Phe Glu Ser Asp Asn Ile Gly Asp Trp Val Ile Val Lys Lys Asp Gly

180

185

190

Val Pro Thr Tyr Asn Phe Ala Val Ala Val Asp Asp His Tyr Met Gln  
 195 200 205

Ile Ser Asp Val Ile Arg Gly Asp Asp His Val Ser Asn Thr Pro Lys  
 210 215 220

Gln Leu Met Ile Tyr Glu Ala Phe Gly Trp Glu Ala Pro Arg Phe Gly  
 225 230 235 240

His Met Ser Leu Ile Val Asn Glu Glu Arg Lys Lys Leu Ser Lys Arg  
 245 250 255

Asp Gly Gln Ile Leu Gln Phe Ile Glu Gln Tyr Arg Asp Leu Gly Tyr  
 260 265 270

Leu Pro Glu Ala Leu Phe Asn Phe Ile Thr Leu Leu Gly Trp Ser Pro  
 275 280 285

Glu Gly Glu Glu Glu Ile Phe Ser Lys Glu Glu Phe Ile Lys Ile Phe  
 290 295 300

Asp Glu Lys Arg Leu Ser Lys Ser Pro Ala Met Phe Asp Arg Gln Lys  
 305 310 315 320

Leu Ala Trp Val Asn Asn Gln Tyr Met Lys Thr Lys Asp Thr Glu Thr  
 325 330 335

Val Phe Glu Leu Ala Leu Pro His Leu Ile Lys Ala Asn Leu Ile Pro  
 340 345 350

Glu Asn Pro Ser Glu Lys Asp Arg Glu Trp Gly Arg Lys Leu Ile Ala  
 355 360 365

Leu Tyr Gln Lys Glu Met Ser Tyr Ala Gly Glu Ile Val Pro Leu Ser  
 370 375 380

Glu Met Phe Phe His Glu Met Pro Glu Leu Gly Lys Asp Glu Gln Glu  
 385 390 395 400

Val Leu Gln Gly Glu Gln Val Pro Glu Leu Met Asn His Leu Tyr Gly  
 405 410 415

Lys Leu Glu Ser Leu Glu Ser Phe Glu Ala Thr Glu Ile Lys Lys Met  
 420 425 430

Ile Lys Glu Val Gln Lys Glu Thr Gly Ile Lys Gly Lys Gln Leu Phe  
435 440 445

Met Pro Ile Arg Val Ala Val Thr Gly Gln Met His Gly Pro Glu Leu  
450 455 460

Pro Asn Thr Ile Glu Val Leu Gly Lys Asp Lys Val Leu Ser Arg Leu  
465 470 475 480

Lys Asn Leu Val

<210> 54  
<211> 296  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 54

Met Glu Tyr Lys Asp Ile Ala Thr Pro Ser Arg Thr Arg Ala Leu Leu  
1 5 10 15

Asp Gln Tyr Gly Phe Asn Phe Lys Lys Ser Leu Gly Gln Asn Phe Leu  
20 25 30

Ile Asp Val Asn Ile Ile Asn Lys Ile Ile Glu Ala Ser His Ile Asp  
35 40 45

Cys Thr Thr Gly Val Ile Glu Val Gly Pro Gly Met Gly Ser Leu Thr  
50 55 60

Glu Gln Leu Ala Lys Asn Ala Lys Lys Val Met Ala Phe Glu Ile Asp  
65 70 75 80

Gln Arg Leu Ile Pro Val Leu Lys Asp Thr Leu Ser Pro Tyr Asp Asn  
85 90 95

Val Thr Ile Ile Asn Glu Asp Ile Leu Lys Ala Asp Ile Ala Lys Ala  
100 105 110

Val Asp Thr His Leu Gln Asp Cys Asp Lys Ile Met Val Val Ala Asn  
115 120 125

Leu Pro Tyr Tyr Ile Thr Thr Pro Ile Leu Leu Asn Leu Met Gln Gln  
130 135 140

Asp Val Pro Ile Asp Gly Phe Val Val Met Met Gln Lys Glu Val Gly  
145 150 155 160

Glu Arg Leu Asn Ala Gln Val Gly Thr Lys Ala Tyr Gly Ser Leu Ser  
165 170 175

Ile Val Ala Gln Tyr Tyr Glu Thr Ser Lys Val Leu Thr Val Pro  
180 185 190

Lys Thr Val Phe Met Pro Pro Asn Val Asp Ser Ile Val Val Lys  
195 200 205

Leu Met Gln Arg Gln Glu Pro Leu Val Gln Val Asp Asp Glu Glu Gly  
210 215 220

Phe Phe Lys Leu Ala Lys Ala Ala Phe Ala Gln Arg Arg Lys Thr Ile  
225 230 235 240

Asn Asn Asn Tyr Gln Asn Phe Phe Lys Asp Gly Lys Lys Asn Lys Glu  
245 250 255

Thr Ile Arg Gln Trp Leu Glu Ser Ala Gly Ile Asp Pro Lys Arg Arg  
260 265 270

Gly Glu Thr Leu Thr Ile Gln Asp Phe Ala Thr Leu Tyr Glu Gln Lys  
275 280 285

Lys Lys Phe Ser Glu Leu Thr Asn  
290 295

<210> 55

<211> 106

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 55

Met Thr Ser Asn His His Ala Pro Tyr Asp Leu Gly Tyr Thr Arg Ala  
1 5 10 15

Thr Met Asp Asn Thr Lys Gly Ser Glu Thr Ala Arg Ser Ser Lys Ser  
20 25 30

His Lys Val Val Leu Ser Ser Asp Cys Ser Leu Gln Leu Asp Tyr Met  
35 40 45

Lys Leu Glu Ser Leu Val Ile Val Asp Gln His Ala Thr Val Asn Thr  
50 55 60

Phe Pro Gly Leu Val His Thr Ala Arg His Thr Thr Arg Val Cys Asn  
65 70 75 80

Thr Arg Ser Arg Trp Ser Asn His Leu Glu Leu Ala Val Glu Gly Gly  
85 90 95

Thr Asn Asp Trp Gly Glu Val Val Thr Arg  
100 105

<210> 56  
<211> 442  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 56

Met Phe Phe Lys Gln Phe Tyr Asp Lys His Leu Ser Gln Ala Ser Tyr  
1 5 10 15

Leu Ile Gly Cys Gln Lys Thr Gly Glu Ala Met Ile Ile Asp Pro Ile  
20 25 30

Arg Asp Leu Ser Ser Tyr Ile Arg Val Ala Asp Glu Glu Gly Leu Thr  
35 40 45

Ile Thr His Ala Ala Glu Thr His Ile His Ala Asp Phe Ala Ser Gly  
50 55 60

Ile Arg Asp Val Ala Ile Lys Leu Asn Ala Ser Ile Tyr Val Ser Gly  
65 70 75 80

Glu Ser Asp Asp Thr Leu Gly Tyr Lys Asn Met Pro Asn Gln Thr His  
85 90 95

Phe Val Gln His Asn Asp Asp Ile Tyr Val Gly Asn Ile Lys Leu Lys  
100 105 110

Val Leu His Thr Pro Gly His Thr Pro Glu Ser Ile Ser Phe Leu Leu  
115 120 125

Thr Asp Glu Gly Ala Gly Ala Gln Val Pro Met Gly Leu Phe Ser Gly  
130 135 140

Asp Phe Ile Phe Val Gly Asp Ile Gly Arg Pro Asp Leu Leu Glu Lys  
145 150 155 160

Ala Val Lys Val Glu Gly Ser Ser Glu Ile Gly Ala Lys Gln Met Phe  
165 170 175

Lys Ser Ile Glu Ser Ile Lys Asp Leu Pro Asn Tyr Ile Gln Ile Trp  
180 185 190

Pro Gly His Gly Ala Gly Ser Pro Cys Gly Lys Ser Leu Gly Ala Ile  
195 200 205

Pro Thr Ser Thr Leu Gly Tyr Glu Lys Gln Thr Asn Trp Ala Phe Ser  
210 215 220

Glu Asn Asn Glu Ala Thr Phe Ile Asp Lys Leu Ile Ser Asp Gln Pro  
225 230 235 240

Ala Pro Pro His His Phe Ala Gln Met Lys Lys Ile Asn Gln Phe Gly  
245 250 255

Met Asn Leu Tyr Gln Pro Tyr Thr Val Tyr Pro Ala Thr Asn Thr Asn  
260 265 270

Arg Leu Thr Phe Asp Leu Arg Ser Lys Glu Ala Tyr His Gly Gly His  
275 280 285

Ile Glu Gly Thr Ile Asn Ile Pro Tyr Asp Lys Asn Phe Ile Asn Gln  
290 295 300

Ile Gly Trp Tyr Leu Asn Tyr Asp Gln Glu Ile Asn Leu Ile Gly Glu  
305 310 315 320

Tyr His Leu Val Ser Lys Ala Thr His Thr Leu Gln Leu Ile Gly Tyr  
325 330 335

Asp Asp Val Ala Gly Tyr Gln Leu Pro Gln Ser Lys Ile Gln Thr Arg  
340 345 350

Ser Ile His Ser Glu Asp Ile Thr Gly Asn Glu Ser His Ile Leu Asp  
355 360 365

Val Arg Asn Asp Asn Glu Trp Asn Asn Gly His Leu Ser Gln Ala Val  
370 375 380

His Val Pro His Gly Lys Leu Leu Glu Thr Asp Leu Pro Phe Asn Arg  
385 390 395 400

Asn Asp Val Ile Tyr Val His Cys Gln Ser Gly Ile Arg Ser Ser Ile

405

410

415

Ala Ile Gly Ile Leu Glu His Lys Gly Tyr His Asn Ile Ile Asn Val  
420 425 430

Asn Glu Gly Tyr Lys Asp Ile His Leu Ser  
435 440

<210> 57  
<211> 285  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 57

Leu Lys Lys Ile Leu Val Leu Ser Leu Thr Ala Phe Leu Val Leu Ala  
1 5 10 15

Gly Cys Asn Ser Gly Asp Lys Thr Asp Thr Lys Asp Lys Lys Glu Glu  
20 25 30

Thr Lys Gln Thr Ser Lys Ala Asn Lys Glu Asn Lys Glu Gln His His  
35 40 45

Lys Gln Glu Asn Asp Asn Lys Ala Ser Thr Gln Leu Ser Glu Lys Glu  
50 55 60

Arg Leu Ala Leu Ala Phe Tyr Ala Asp Gly Val Glu Lys Tyr Met Leu  
65 70 75 80

Thr Lys Asn Glu Val Leu Thr Gly Val Tyr Asp Tyr Gln Lys Gly Asn  
85 90 95

Glu Thr Glu Lys Lys Gln Met Glu Gln Leu Met Leu Glu Lys Ala Asp  
100 105 110

Ser Met Lys Asn Ala Pro Lys Asp Met Lys Phe Tyr Gln Val Tyr Pro  
115 120 125

Ser Lys Gly Gln Phe Ala Ser Ile Val Gly Val Asn Lys Asn Lys Ile  
130 135 140

Phe Ile Gly Ser Thr Gln Gly Ala Leu Ile Asp Tyr Gln Thr Leu Leu  
145 150 155 160

Asn Asn Gly Lys Glu Leu Asp Ile Ser Gln Leu Tyr Glu Asp Asn Lys  
165 170 175

Asp Asn Arg Ser Leu Glu Glu Met Lys Asn Lys Ile Glu Ile Val Asp  
180 185 190

Ser Gly Ala Ala Gln Lys Ala Asp Asp Pro Asp Lys Asn Ser Ala Asn  
195 200 205

Thr Met Ala His Met Arg Ser Gln Ile Tyr Glu Lys Ile Ser Asp Phe  
210 215 220

Asp Gly Lys Leu Asp Asn Lys Thr Tyr Leu Trp Asp Asn Ile Arg Ile  
225 230 235 240

Asn Asp Asp Gly Asn Trp Thr Val His Tyr Arg Asn His Asp Gly Glu  
245 250 255

Ile Met Gly Thr Tyr Lys Ser Glu Lys Asn Lys Ile Ile Lys Leu Asp  
260 265 270

Gln Asn Gly Asn Lys Ile Lys Glu Gln Gln Met Ser Asn  
275 280 285

<210> 58  
<211> 498  
<212> PRT  
<213> Staphylococcus epidermidis

<400> 58

Met Ala Asn Lys Glu Ser Lys Asn Val Val Ile Ile Gly Ala Gly Val  
1 5 10 15

Leu Ser Thr Thr Phe Gly Ser Met Ile Lys Glu Leu Glu Pro Asp Trp  
20 25 30

Asn Ile Lys Leu Tyr Glu Arg Leu Asp Arg Pro Gly Ile Glu Ser Ser  
35 40 45

Asn Glu Arg Asn Asn Ala Gly Thr Gly His Ala Ala Leu Cys Glu Leu  
50 55 60

Asn Tyr Thr Val Gln Gln Pro Asp Gly Ser Ile Asp Ile Glu Lys Ala  
65 70 75 80

Lys Glu Ile Asn Glu Gln Phe Glu Ile Ser Lys Gln Phe Trp Gly His  
85 90 95

Leu Val Lys Ser Gly Asn Ile Ser Asn Pro Arg Asp Phe Ile Asn Pro

100 105 110

Leu Pro His Ile Ser Phe Val Arg Gly Lys Asn Asn Val Lys Phe Leu  
115 120 125

Lys Asn Arg Tyr Glu Ala Met Arg Asn Phe Pro Met Phe Asp Asn Ile  
130 135 140

Glu Tyr Thr Glu Asp Ile Glu Glu Met Arg Lys Trp Met Pro Leu Met  
145 150 155 160

Met Thr Gly Arg Thr Gly Asn Glu Ile Met Ala Ala Ser Lys Ile Asp  
165 170 175

Glu Gly Thr Asp Val Asn Tyr Gly Glu Leu Thr Arg Lys Met Ala Lys  
180 185 190

Ser Ile Glu Lys His Pro Asn Ala Asp Val Gln Tyr Asn His Glu Val  
195 200 205

Ile Asn Phe Asn Arg Arg Lys Asp Gly Ile Trp Glu Val Lys Val Lys  
210 215 220

Asn Arg Asn Ser Gly Asp Val Glu Thr Val Leu Ala Asp Tyr Val Phe  
225 230 235 240

Ile Gly Ala Gly Gly Ala Ile Pro Leu Leu Gln Lys Thr Gly Ile  
245 250 255

Pro Glu Ser Lys His Leu Gly Gly Phe Pro Ile Ser Gly Gln Phe Leu  
260 265 270

Ile Cys Thr Asn Pro Asp Val Ile Asn Glu His Asp Val Lys Val Tyr  
275 280 285

Gly Lys Glu Pro Pro Gly Thr Pro Pro Met Thr Val Pro His Leu Asp  
290 295 300

Thr Arg Tyr Ile Asp Gly Glu Arg Thr Leu Leu Phe Gly Pro Phe Ala  
305 310 315 320

Asn Ile Gly Pro Lys Phe Leu Arg Asn Gly Ser Asn Leu Asp Leu Phe  
325 330 335

Lys Ser Val Lys Pro Tyr Asn Ile Thr Thr Leu Leu Ala Ser Ala Val  
340 345 350

Lys Asn Leu Pro Leu Ile Lys Tyr Ser Ile Asp Gln Val Leu Met Thr  
355 360 365

Lys Glu Gly Cys Met Asn His Leu Arg Thr Phe Tyr Pro Glu Ala Arg  
370 375 380

Asp Glu Asp Trp Gln Leu Tyr Thr Ala Gly Lys Arg Val Gln Val Ile  
385 390 395 400

Lys Asp Thr Lys Glu His Gly Lys Gly Phe Ile Gln Phe Gly Thr Glu  
405 410 415

Val Val Asn Ser Lys Asp His Ser Val Ile Ala Leu Leu Gly Glu Ser  
420 425 430

Pro Gly Ala Ser Thr Ser Val Ser Val Ala Leu Glu Val Leu Glu Lys  
435 440 445

Asn Phe Ala Glu Tyr Glu Lys Asp Trp Thr Pro Lys Leu Gln Lys Met  
450 455 460

Ile Pro Ser Tyr Gly Lys Ser Leu Ile Asp Asp Val Lys Leu Met Arg  
465 470 475 480

Ala Thr Arg Lys Gln Thr Ser Lys Asp Leu Glu Leu Asn Tyr Tyr Glu  
485 490 495

Ser Lys

<210> 59  
<211> 516  
<212> PRT  
<213> *Staphylococcus epidermidis*  
<400> 59

Met Lys Ile Phe Lys Thr Leu Ser Ser Ile Leu Val Thr Ser Val Leu  
1 5 10 15

Ser Val Thr Val Ile Pro Ser Thr Phe Ala Ser Thr Glu Ser Thr Ala  
20 25 30

Thr Asn Gln Thr Gln Gln Thr Val Leu Phe Asp Asn Ser His Ala Gln  
35 40 45

Thr Ala Gly Ala Ala Asp Trp Val Ile Asp Gly Ala Phe Ser Asp Tyr  
50 55 60

Ala Asp Ser Met Arg Lys Gln Gly Tyr Gln Val Lys Glu Leu Glu Gly  
65 70 75 80

Glu Ser Asn Ile Ser Asp Gln Ser Leu Gln Gln Ala His Val Leu Val  
85 90 95

Ile Pro Glu Ala Asn Asn Pro Phe Lys Glu Asn Glu Gln Lys Ala Ile  
100 105 110

Ile Asn Phe Val Lys Asn Gly Gly Ser Val Ile Phe Ile Ser Asp His  
115 120 125

Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile Asp Ser Ser Glu Ser Met  
130 135 140

Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asn Met Thr Lys Asp Met Asn  
145 150 155 160

Asn Glu Glu Lys Asn Ser Asn Val Met His Asn Val Lys Ser Ser Asp  
165 170 175

Trp Leu Ser Gln Asn Phe Gly Val Arg Phe Arg Tyr Asn Ala Leu Gly  
180 185 190

Asp Ile Asn Thr Gln Asn Ile Val Ser Ser Lys Asp Ser Phe Gly Ile  
195 200 205

Thr Lys Gly Val Gln Ser Val Ser Met His Ala Gly Ser Thr Leu Ala  
210 215 220

Ile Thr Asp Pro Asn Lys Ala Lys Gly Ile Ile Tyr Met Pro Glu His  
225 230 235 240

Leu Thr His Ser Gln Lys Trp Pro His Ala Val Asp Gln Gly Ile Tyr  
245 250 255

Asn Gly Gly Ile Asn Glu Gly Pro Tyr Val Ala Ile Ser Lys Ile  
260 265 270

Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp Ser Ser Leu Val Glu Asp  
275 280 285

Arg Ser Pro Lys Tyr Leu Arg Glu Asp Asn Gly Lys Pro Lys Lys Thr

290

295

300

Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly Lys Leu Leu Asn Asn Leu  
305 310 315 320

Thr Thr Trp Leu Gly Lys Lys Glu Ser Gln Ser Ser Met Lys Asp Met  
325 330 335

Gly Ile Lys Leu Asp Asn Lys Thr Pro Leu Leu Asn Phe Glu Gln Pro  
340 345 350

Glu Asn Ser Ile Glu Pro Gln Lys Glu Pro Trp Thr Asn Pro Ile Glu  
355 360 365

Gly Tyr Lys Trp Tyr Asp Arg Ser Thr Phe Lys Thr Gly Ser Tyr Gly  
370 375 380

Ser Asn Gln Arg Gly Ala Asp Asp Gly Val Asp Asp Lys Ser Ser Ser  
385 390 395 400

His Gln Asn Gln Asn Ala Lys Val Glu Leu Thr Leu Pro Gln Asn Ile  
405 410 415

Gln Pro His His Pro Phe Gln Phe Thr Ile Lys Leu Thr Gly Tyr Glu  
420 425 430

Pro Asn Ser Thr Ile Ser Asp Val Arg Val Gly Leu Tyr Lys Asp Gly  
435 440 445

Gly Lys Gln Ile Gly Ser Phe Ser Ser Asn Arg Asn Gln Phe Asn Thr  
450 455 460

Leu Gly Tyr Ser Pro Gly Gln Ser Ile Lys Ala Asn Gly Ala Gly Glu  
465 470 475 480

Ala Ser Phe Thr Leu Thr Ala Lys Val Thr Asp Glu Ile Lys Asp Ala  
485 490 495

Asn Ile Arg Val Lys Gln Gly Lys Lys Ile Leu Leu Thr Gln Lys Met  
500 505 510

Asn Glu Asn Phe  
515

<210> 60  
<211> 84

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 60

Gly Thr Pro Leu Glu Leu Val Phe Val Asn Thr Leu Gly Pro Lys Pro  
1 5 10 15

Cys Phe Ala Lys Pro Asn Lys Ile Leu Leu Glu Tyr Ile Pro Leu  
20 25 30

Phe Val Ala Asp Ala Ala Val Lys Thr Thr Lys Leu Thr Met Pro  
35 40 45

Ala Ala Lys Gly Thr Pro Ile Ser Val Asn Asn Leu Thr Asn Gly Leu  
50 55 60

Leu Ser Gly Ser Thr Leu Asn His Gly Met Thr Asp Met Ile Thr Ser  
65 70 75 80

Lys Pro Pro Ile

<210> 61

<211> 54

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 61

Ser Ser Leu Ser Thr Ile Ile Pro Phe Ser Leu Gly Ala Leu Gly Lys  
1 5 10 15

Phe Asn Ser Phe Ile Glu Gln Ile Ile Pro Leu Glu Ser Thr Pro Arg  
20 25 30

Asn Trp Ala Ser Leu Ile Thr Ile Pro Leu Gly Ile Thr Ala Pro Thr  
35 40 45

Phe Ala Thr Thr Thr Phe  
50

<210> 62

<211> 116

<212> PRT

<213> *Staphylococcus aureus*

<400> 62

Met Lys Phe Lys Lys Tyr Ile Leu Thr Gly Thr Leu Ala Leu Leu Leu  
1 5 10 15

Ser Ser Thr Gly Ile Ala Thr Ile Glu Gly Asn Lys Ala Asp Ala Ser  
20 25 30

Ser Leu Asp Lys Tyr Leu Thr Glu Ser Gln Phe His Asp Lys Arg Ile  
35 40 45

Ala Glu Glu Leu Arg Thr Leu Leu Asn Lys Ser Asn Val Tyr Ala Leu  
50 55 60

Ala Ala Gly Ser Leu Asn Pro Tyr Tyr Lys Arg Thr Ile Met Met Asn  
65 70 75 80

Glu Tyr Arg Ala Lys Ala Ala Leu Lys Lys Asn Asp Phe Val Ser Met  
85 90 95

Ala Asp Ala Lys Val Ala Leu Glu Lys Ile Tyr Lys Glu Ile Asp Glu  
100 105 110

Ile Ile Asn Arg  
115

<210> 63  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 63  
Lys Leu Lys Leu Leu Leu Lys Leu Lys  
1 5 10

<210> 64  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 64  
Arg Leu Ala Gly Leu Leu Arg Lys Gly Gly Glu Lys Ile Gly Glu Lys  
1 5 10 15

Leu Lys Lys Ile Gly Gln Lys Ile Lys Asn Phe Phe Gln Lys Leu Val  
20 25 30

Pro Gln Pro Glu  
35